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November 5, 2003, 20:06:21; Search time 46.4249 Seconds (without alignments) 875.264 Million cell updates/sec
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1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description
-	1335	100.0	:	22	AAB81128	C17E2 OspA constru
7	1335	100.0		23	AAU97869	E. coli codon opti
٣	832	62.3		22	AAB81127	Optimised OspA pro
4	832	62.3		23	AAU97868	Escherichia coli c
S	815	61.0			AAG78025	Piscirickettsia sa
ø	815	61.0		22	AAB81126	OspA antigen amino
7	815	61.0	162		AAU97867	Piscirickettsia sa
œ	487	36.5		22	AAE05746	Clostridium cellul
σ	487	36.5			AAE05749	Chimeric S peptide

99CA-2281913. 99CA-2281913

17-SEP-1999; 17-SEP-1999;

17-MAR-2001.

FFX8X8X4X

CA2281913-A1

011	83 3	2.2.5	341	15	AAE05747 AAR63634	Clos Cell	Clostridium cellul Cellulose binding
	m m	2.5	163 428	7 7 7 7 7 7 7	AAE05745 AAE05748	Clos	stridium cellul stridium cellul
	m	0.9	382	50	AAY39952	Gaussi	ssia luciferase
15 480.5	m r	0.0	382	53	AAE13383	Gaussi	sia species CB
	n m	5.4	154	202	AAW90081	; _C	ellulovorans C
	σ,	4.6	156	20	AAW90080	5	ellulovorans C
		20 α 4. 4	167	27	AAR95080 AAY54123	Cell	ulose binding
		. 4.	493	50	AAY28850	Pect	Pectate lyase-link
	н,	4.8	493	50	AAY43218	Pect	ate lyase CBD
	-	4.4	531	18	AAW15238	Scal	toldin protein
	4 ~	7.7	1426	50	AAY13492	Tru	netmocerium ce ncated cellulas
	т.	1.2	1426	23	AAE16323	Acti	ive cellulase p
			616	200	AAY13494	Tru	ncated cellulas
		7.7	1751	7 0	AAY13493	Trut	lve cellulase n cated cellulas
	-	1.1	1751	23	AAE16324	Acti	ive cellulase p
		9.0	182	24	ABJ18820	Pset	Pseudomonas aerugi
		, o	1350	7 2	AAG63962 AAG63963	Amir	Amino acid sequenc
		9.3	153	24	ABP71658	A.	cellulolyticus
		e. 6	1121	24	ABP71656	A. C.	sellulolyticus
		7.0	150	1 B	AAW18/90 ABD73025	Amino	Corrected Bacilius
		1.6	1228	24	ABP73029	Amino	acid
		0.6	154	24	ABP73020	Amino	acid
		0.0	762		ABP73022	Amino	acid
		۰.0	0 0		ABP/3018	Amino	acid
		. w . w	477	2 4	ABE / 301 / AAO 22444	Amino	acid seque in encoded
		9.6	496	23	AA022443	Prot	in encoded
		9.	677	23	AAU98063	Bacı	Bacillus subtilis
					ALIGNMENTS		
RESULT 1 AAB81128 ID AAB8112	ω	standard;	Protein		256 AA.		
X C AAB8112	8;						
11-JUL	-2001	(first	t entry)	ŝ			
C17E2	OspA co	construct		h -N	with N-terminal fusion	partner.	
XX KW Poikilothermic KW vaccine; OspA;			h; Pis monid	ciri rick	fish, Piscirickettsia salmonis, r salmonid rickettsial septicaemia,	ickettsial rickettsi	pathogen; al disease;
		Blon	rusion construct	uct.			
	Piscirickettsia Synthetic.		salmonis	٠			
		Š,	cation	/Qua	Location/Qualifiers		
		:47	abel=	Unde	Undefined_N-terminal	_fusion_partner	t,
T Keglon		, , ,	96256 /label= /note= "	C17E2 Os Product	2 OspA uct of OspA gene	optimised for	expression in
T.A.				Esch	Escherichia coli"		

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RESULT 3
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                                                                                                                                                                                                This invention relates to a method for the protection against infection of a poixllothermic fish by the bacterial pathogen, Piscirickettsia samionis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of 05pA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGNSYVDNTSKVTANFVKETASPTSTYDDFYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                       Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKVKAGQVTRWRNPDJTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKVKAGGVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAM1AGQKQE1YGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%; Score 1335; DB 22; Length 256; Local Similarity 100.0%; Pred. No. 9.1e-123; es 256; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU97869 standard; Protein; 256 AA.
                                                                                                                                                                           Example 4; Fig 5; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia salmonis
                                                                                    WPI; 2001-316844/34.
N-PSDB; AAF86248.
                                                            Burian J,
                                   KUZYK M A.
                       BURIAN J
          KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 256;
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                      (BURI/)
                                                           Kay WW,
          (KAYW/)
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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprocein), its variants, non-lipidated form or antigenic method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related in fin-fish against Rickettsial septicaemia and other related This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) with an N-terminal fusion used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                    Kuzyk MA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 5; 55pp; English.
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                                                                                                                     19-MAR-2001; 2001CA-2339327.
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                                                                                                                                                                                                                                                                                                                                                                                                 Thornton JC, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain, as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-455221/49.
                                                                                                                                                                                                                                              THORNTON J
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                                                                                                                                                                                                                                                                        (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
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CA2339327-A1
                                                            15-MAR-2002
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9 9

Synthetic

Region

Key

(BURI/) E

Kay WW,

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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsial salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                          Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
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100.0%; Pred. No. 1.4e-73;
iive 0; Mismatches 0;
                                                               Escherichia coli codon optimised OspA, 17e2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian J, Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 5; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2000; 2000US-0677374.
                     12-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 161; Conservative
                                                                                                                                                                                                      Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain, as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-455221/49.
N-PSDB; ABK52402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thornton JC,
                                                                                                                                                                                                                                                                      CA2339327-A1.
                                                                                                                                                                                                                                                                                                                   15-MAR-2002.
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAYW/)
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ID AAG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a method for the protection against infection of a poixlothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 08pA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkliothermic fish, against the bacterial pathogen P. Salmonis. The method is also useful for protecting against salmickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 1772. The DNA encoding OspA 1782 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for protecting poikilothermic fish against salmonid rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                        Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 RRQOYCREFQOKAMIAGOKQEIYGTACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Optimised OspA protein 17E2 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 1.4
Matches 161; Conservative 0; Mismatches
                                                                                                                                                                                                                            109..128
/label= B_cell_epitope
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97868 standard; Protein; 161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                   99CA-2281913
                                                                                                                                    Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF86247
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                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
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Gaps

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Length 161; Indels

Sequence

Query Match

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AAU97868

AAU97868 ID AAU9 XX AC AAU9

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AAG78025

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents P. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine, OspA; salmonid rickettsial septicaemia, rickettsial disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 815; DB 22;
Pred. No. 6.4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                110..129
/label= B_cell_epitope
                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 2B; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%;
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                                                         salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                                      Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                           (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF86246
                                                         Piscirickettsia
                                                                                                                                                                                                                                                   17-SEP-1999;
                                                                                                                                                                                                                                                                                     17-SEP-1999;
                                                                                                                                                                        CA2281913-A1
                                                                                                                                                                                                              17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 158;
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                                                                                                 Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RGCLÓGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acid sequences and the encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;
                                                                                               Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial;
septicaemia; SRS; surface antigen; vaccine; antibacterial; fish;
ATCC VR-1361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valenzuela P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 815; DB 22;
Pred. No. 6.4e-72;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths S,
                                                                             Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OspA antigen amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 5; 25pp; English.
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                01-JUL-2000; 2000GB-0016080.
01-JUL-2000; 2000GB-0016082.
29-JUL-2000; 2000GB-0018599.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (AQUA-) AQUA HEALTH EURO LTD
                                                                                                                                                                                                                                                                                                                                                2000GB-0005838.
                                                                                                                                                                                                                                                                                                         12-MAR-2001; 2001WO-GB01055
                                         (first entry)
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                                                                                                                                                                                            Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639050/73.
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Best Local Similarity
Matches 158; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH79040.
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                                                                                                                                                                                                                                                                                                                                                11-MAR-2000;
                                       15-JAN-2002
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Simard N, Burzio L;

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Sequence

AAB81126;

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The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming steep in fluting paper manufacture
which eliminates the sizing steep. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNSYVDNTSKVTANFVKETASPĮSTYDĮYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GRITKSDWSNYTQTNDYSFDASSSTPVVNP------KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
  Polysaccharide modification; polysaccharide binding domain; PBD; paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present requence is Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids of C. cellulovorans CBD (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE------
                  yarn; fiber; textile; biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KKGOFITIO----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.5%; Score 487; DB 22;
46.8%; Pred. No. 1.4e-39;
7ative 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                     (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1.2; Fig 1e-1g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 Shoseyov 0;
                                                                                                                                                                                                                                                                            99US-0164140.
                                                                                                                                                                                                                                     02-NOV-2000; 2000WO-IL00708
                                                                                                                  Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Nussinovitch A,
                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-457121/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       penetrate paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD11043
                                                                                                                                                         WO200134091-A2
                                                                                                                                                                                                                                                                            08-NOV-1999;
                                                                                                                                                                                                                                                                                                 18-NOV-1999;
                                                                                                                                                                                                17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   Levy I,
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYKVKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium cellulovorans cellulose binding domain-180 (CBD-180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODYCREFORKAMIAGOKOEIYGTACROPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 815; DB 23;
Pred. No. 6.4e-72;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                              Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05746 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                              Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%;
98.8%;
                                                                                                                                                                                              19-MAR-2001; 2001CA-2339327
                                                                                                                                                                                                                                     15-SEP-2000; 2000US-0677374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                             Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                            Thornton JC, Kay WW,
                                      Rickettisial disease.
                                                                                                                                                                                                                                                                            (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain, as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                   2002-455221/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 158; Conserv
                                                                                                                                                                                                                                                                                               (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK52401
                                                                                                                  CA2339327-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2001
                                                                                                                                                         15-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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9

Gaps

90;

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Nussinovitch A, Shoseyov O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE05747;
                                                                                                            Seguence
                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy I,
 which
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE05747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in fluting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
/note= "Encoded by TAG"
327...38
/note= "These residues are absent in the sequence shown
as SEQ ID NO: 10 in the sequence listing"
                                                                                                                                                                                   Polysaccharide modification; polysaccharide binding domain; PBD; paper;
                                                                                                                                                                                                                                                                                                        30..208
/note= "This region is derived from C. cellulovorans"
                                                                                                                                                                                              yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD; chimeric protein; S peptide-cellulose binding domain-S protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                               226..326
/note= "This region is derived from bovine"
                                                                                                                                                           Chimeric S peptide-cellulose binding domain-S protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy I, Nussinovitch A, Shoseyov O;
                                                                                                                                                                                                                                                      Chimeric - Clostridium cellulovorans
Chimeric - Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 4b-4g; 121pp; English
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                   AAE05749 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000; 2000WO-IL00708
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                   Spep-CBD-Sprot; bovine
 GTACPQPD 246
                        154 GTA-PGPD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-457121/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB, AAD11046
                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-1999;
                                                                                                                                   24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001
                                                                                                           AAE05749;
 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           property
                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                Region
                                                                        AAE057
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The present sequence is S peptide-cellulose binding domain-S protein (Spep-CBD-Sprot), a fusion protein derived from Clostridium cellulovorans and bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVKAGQVTR---WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP------KVTGYIGGAK--VL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polysaccharide modification, polysaccharide binding domain, PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------KKĠÒFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue is absent in the sequence shown
                                                                                                                                                     Note: This sequence is stated to be the same as that shown as SEQ ID NO: 10 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                    30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium cellulovorans CBD cross linker protein (CCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as SEQ ID NO: 6 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                     7 Match 36.5%; Score 487; DB 22; Local Similarity 46.8%; Pred. No. 3.1e-39; Les 116; Conservative 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Encoded by CCAIAGGAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE05747 standard; Protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0164140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wet strength; durability;
CBD cross linker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 340..341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTACPQPD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTA-PGPD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 341
                                                                                                                                                                                                                                                                                            328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200134091-A2
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18-NOV-1999;
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WO9424158-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                            Doi RH,
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                                                                                                                                       The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in fluting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
comproves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurxy therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                         strong alkaline conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGNSYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 EKVKAGOVTR--WRNPDIGNSYSVEPVRIYQRYNKQERROOYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 -----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-------KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                       Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 341; Score 487; DB 22; Length 341; Best Local Similarity 46.8%; Pred. No. 3.3e-39; Matches 116; Conservative 12; Mismatches 30; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is Clostridium cellulovorans cellulose binding domain (CBD) cross linker protein (CCP).

Note: This sequence is stated to be the same as that shown as SEQ ID NO: 6 in the sequence listing of the specification. However this sequence has an additional residue at its C-terminal.
                                                                                                                Example 1.2; Fig 2b-2e; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR63634 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose binding domain; CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium cellulovorans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 GTA-PGPD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 GTACPQPD 246
             2001-457121/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 AA;
            WPI; 2001-457121/
N-PSDB; AAD11044.
                                                                                                                                                                                                                                                                                                                                                                       penetrate paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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hids crystalline with a Kd ranging from 1.5 microM - 0.5 microM, binds crystalline with a Kd ranging from 1.5 microM - 0.5 microM, core with a Kd ranging from 1.5 microM - 0.5 microM, core with a Kd calline, with a Kd ranging from 1.5 microM - 0.5 microM, core with a Kd callined, as is a CBD fusion protein and comprising the CBD and a second protein. The second protein is pref. Protein A, heparinase, a hormone or an enzyme capable of degrading an environmental pollutant, or an HSP, HSP antibody, cross-reactive HSP-related protein or an antigenic portion of this. The CBD and FP may be used in drug delivery, affinity septs. and diagnostic techniques. CBD nucleic acid may be obted, from a variety of cell sources that produce CBDs that bind with high affinity and in a reversible manner or that produce CBD encoding mRNA. The preferred (Updated on 25-MAR-2003 to correct FN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated cellulose binding domain and fusion proteins - with applications. including drug delivery, affinity separations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium cellulovorans cellulose binding domain (CBDclos).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KKĞÖFITIÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 483; DB 15;
51.7%; Pred. No. 2.8e-39;
iive 9; Mismatches 14;
                                                                                                                                                                                                                                                                     Shpiegl I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FGFASGRATL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GRITKSDWSNYTQTNDYSFD 136
                                                                                                                                                                                                                                                                     Shoseyov O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05745 standard; Protein; 163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 125pp; English.
                                                          94WO-US04132
                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
(YISS ) YISSUM RES & DEV CO.
                                                                                                                  93US-0048164
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Matches 106; Conservative
                                                                                                                                                                                                                                                                  Goldstein MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic techniques
                                                                                                                                                                                                                                                                                                                          WPI; 1994-341767/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ72917
                                                       14-APR-1994;
                                                                                                                     14-APR-1993;
27-0CT-1994.
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Clostridium cellulovorans protein A-cellulose binding domain.

24-SEP-2001

AAE05748;

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linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) (usion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fine fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
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                                                                                                                                                                                                                                                                     Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTOGOTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Clostridium cellulovorans cellulose binding domain, wet strength; durability; elasticity; CBDClos; cellulose binding protein A; CBP A.
                                                                                                                                                                                                                                                                                                                                               present invention relates to methods and compositions for cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Clostridium cellulovorans cellulose binding domain (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 483; DB 22; Length 163; larity 51.7%; Pred. No. 2.8e-39; Conservative 9; Mismatches 14; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KKGQFITIQ-
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                                                                                                                                                                                    YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                       Example 1.1; Page 111-112; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GRITKSDWSNYTQTNDYSFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                            Shoseyov O;
                                                                                                                                                                       CBDT-) CBD TECHNOLOGIES LTD
                                                                                                                                    99US-0164140.
99US-0166389.
                                                                                                            02-NOV-2000; 2000WO-IL00708
                                     Clostridium cellulovorans.
                                                                                                                                                                                                           Nussinovitch A,
                                                                                                                                                                                                                                  WPI; 2001-457121/49.
N-PSDB; AAD11042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  penetrate paper.
                                                            WO200134091-A2
                                                                                                                                      08-NOV-1999;
                                                                                                                                                18-NOV-1999;
                                                                                    17-MAY-2001
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RESULT 13 AAE05748 ID AAE05748 standard; Protein; 428 AA.

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The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.

The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.

The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in fluting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by TAG"
427..428
/note= "These residues are absent in the sequence shown as SEQ ID NO: 8 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is Clostridium cellulovorans Protein A-cellulose binding domain (ProtA-CBD). This sequence contains a part of CBP A protein and a part of protein A derived from pRIT2T vector sequence. Note: This sequence is stated to be the same as that shown as SEQ ID NO: 8 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                         1..263
/label= Protein A
/note= "This region is derived from pRIT2T vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                       265..426
/label= CBP_A_protein
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                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-2000; 2000WO-IL00708.
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                                                                                                                                                                                                  Clostridium cellulovorans.
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N-PSDB; AAD11045.
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18-NOV-1999;
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                                                                                                                                                         Sequence
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                                                                                                           270 MSVEFYNSNKSAQTNSITPIIKITNISDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 329
                                                                                                                                                                                     361
                                                                                                                                                      61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLAGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                  ----- KKGQFITIQ----- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luciferase; green fluorescent protein; GFP; screening assay; diagnosis; bloluminescence-generating system; toy; cosmetic; fairy dust; beverage; body paint; equirt gun; balloon; slimy play material; soap; toothpaste; fusion protein.
                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTOGOTFWCDHAGAL
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and
Renilla and Ptilosarcus green fluorescent protein nucleic acids -
                                                                                                                                                                                   330 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-------
                                                           16;
                                 Length 428;
                                                              14; Indels
                                Score 483; DB 22;
Pred. No. 1.1e-38;
                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaussia luciferase fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 222-223; 233pp; English.
                                                                                                                                                                                                                                                ------FGFASGRATL-
                                                                                                                                                                                                                                                                             181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                          ----GRITKSDWSNYTQTNDYSFD 400
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                                                                                                                                                                                                                                                                                                                                                                                        AAY39952 standard; Protein; 382
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98US-0089367.
98US-0102939.
                                36.2%;
51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bryan BJ, Szent-Gyorgyi C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                            106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-580443/49.
N-PSDB; AAZ27550.
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(BRYA/) BRYAN B J.
                         Query Match
Best Local Similarity
 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9949019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1998;
15-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1998;
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SQ · Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY39952;
                                                                                                                                                                                                                                                362
                                                                                                                                                                                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaussia
                                                              Matches
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balloons, personal items, dentrifrices, soaps, body paints, bubble bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body powders, body creams, toothpastes, mouthwashes, soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce transgenic fish and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green fluorescent protein; GFP; bioluminescence generating system; toy, luciferase; finger paint; slimy play material; fishing lure; sparkler; doll; balloon; personal care item; cosmetic; bath powder; body cream; tooth paste; mouth wash; soap; body paint; ornamental transgenic plant; bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; ber; wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage; dry ice; textile; clothing; paper product; greeting card; wrapping paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding Renilla reniformis green fluorescent proteins, useful in diagnostic bioluminescence procedures -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%; Score 480.5; DB 20; Length 3
62.6%; Pred. No. 1.7e-38;
ive 10; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaussia species CBD-luciferase fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.0%
Best Local Similarity 62.6%
Matches 107; Conservative
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(BRYA/) BRYAN B J.
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N-PSDB; AAD22201.
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also relates to sequences of the bioluminescence generating system (e.g. luciferase). R. reniformis GFP are used in diagnostic methods and in the production of novelty items such as toys (e.g. squirt gun, pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game toys), finger paints, slimy play material, bubbles in bubble making personal care item (e.g. cosmetic, bath powders, body remans, tooth pastes, mouth wash, soaps, body paints, bubble bath), ornamental transgenic plants, fountain, fairy dust, food (gelatins, icings, transgenic plants, champagne, milk, soft drinks, ice cubes, ice, dry ice, beverage), textile (foot bag, clothing) and/or paper product (greeting cards, wrapping paper). The present sequence is CBD-luciferase fusion protein from Gaussia species.
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Sequence 382 AA;

61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS 120 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60 21; Gaps 118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162 Query Match 36.0%; Score 480.5; DB 23; Length 382; Best Local Similarity 62.6%; Pred. No. 1.7e-38; Matches 107; Conservative 10; Mismatches 33; Indels 21; 엄 ઠ g ò

Search completed: November 5, 2003, 20:12:51 Job time : 47.4249 secs

us-09-677-374-6.rai

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Sequence 22, Appl
                                                                       2003, 20:11:02 ; Search time 16.3592 Seconds (without alignments) 662.108 Million cell updates/sec
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                                                                                                                         US-09-677-374-6
1335
1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
version 5.1.6
- 2003 Compugen Ltd.
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US-08-460-468-2
US-08-460-458-2
US-08-460-458-2
US-08-460-455-2
US-08-006-636-7
US-09-006-632-7
US-09-330-334A-29
US-09-339-1298-4
US-09-339-1298-4
US-09-339-1298-4
US-09-339-1298-4
US-09-339-1298-4
US-09-138-955-13
US-09-138-955-13
US-09-138-955-13
US-09-138-955-13
US-09-634-531-12
US-09-634-531-13
US-09-634-531-13
US-09-634-531-13
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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Match Length
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163
154
156
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Perfect score:
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Sequence 22, Application US/09277716A
; Sequence 22, Application US/09277716A
; Sequence 22, Application US/09277716A
; GENERAL INFORMATION:
; APPLICANT: BYPAN, BULUE
; APPLICANT: Szent-Gyorgy;
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLBIC ACIDS ENCODING THE
; TITLE OF INVENTION: UNMERS: US/09/277,716A
; CURRENT PELLING DATE: 1999-03-26
; CURRENT FILING DATE: 1999-10-01
; BARLIER FILING DATE: 1998-10-01
; BARLIER FILING DATE: 1998-06-15
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTHARE: PELLING UNCE: 2.0
; SEQ ID NO 2.2
LENTH: SACHER PARELLY OF THE PARELY OF THE PARELLY OF THE PARELY OF THE PARELLY OF T
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                                       115, Appl
31960, A
31060, A
7802, Ap
26658, A
26658, A
8009, A
4283, A
4442, Ap
4453, Ap
4453, Ap
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12, Appl
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             Sequence
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US-09-152-911A-11960
US-09-128-352-7068
US-09-328-352-7068
US-09-328-352-7002
US-09-328-352-7802
US-09-328-352-891A-2658
US-09-328-352-891A-26438
US-09-328-352-4423
US-09-328-352-4442
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US-10-09-328-352-4442
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US-10-09-328-352-442
US-09-328-352-442
US-09-328-352-442
US-09-328-352-442
US-09-328-352-4253
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US-09-328-352-4253
US-09-328-352-4253
US-09-3440-319-12
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US-09-609-161B-22
i Sequence 22, Application US/09609161B
i Patent No. 643662
i GENERAL INFORMATION:
i APPLICANT: Bryan, Bruce
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         Best Local Similarity
         RESULT 1
US-09-277-716-22
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         Query Match
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22817, A 1, Appli 19701, A

2, Appli

Sequence Sequence Sequence Sequence

US-09-252-991A-19701 US-09-252-991A-23334 US-07-862-588B-2

616 1751 192 551

Appl

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GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoisegl, Itai
APPLICANT: Shoisegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Pred. No. 3.8e-41;
2; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,462
FILING DATE: CONCURRENTLY herewith
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTONEY/AGENT INPORMATION:
NAME: MISTOCK, S. Lefile
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,972
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGNSYVDNTSKVTANFVKETASPISTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
REFERENCE/DOCKET NUMBER: 7809-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-460-462-2; Sequence 2, Application US/08460462; Patent No. 5670623
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                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.7%;
Best Local Similarity 97.8%;
Matches 90; Conservative
                                                                                                                                                                                                     LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                     TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-048-164A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LID.
TITLE OF INVENTION: LUGIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCTITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGTLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
FILE REFERENCE: 24729-121B
FILE REFERENCE: 24729-121B
FILE REFERENCE: 24729-121B
FILE REFERENCE: 2000-06-30
PRIOR PAPLICATION NUMBER: US/09609,161B
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR PILING DATE: 1999-10-01
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1999-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Cellulose Binding Domain (CBD)-Gaussia luciferase fusion protein
US-09-609-161B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVBFGFASGAATLKKGQFITIQGRITKSDWS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGNSYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IGGAKVLGTAPGS 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFURMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, ROY H. LULOSE BINDING DOMAIN
TITLE OF INVERTION: CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: PATEMET RELABER PC-DOS/MS-DOS
SOFTWARE: PATEMET RELABER
CORPUTER: BATEMET RELABER
SOFTWARE: PATEMET RELABER
PRINCATION NUMBER: US/08/048,164A
BTILNCATION NUMBER: US.A.
BELLINCATION NUMBER: US.A.A.B.-1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence: fusion protein
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08048164A Patent No. 5496934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18,872
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NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-048-164A-2
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RESULT 7
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                                                                      6 MSVEFYNSNKSAQINSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQIFWCDHAGAL 65
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                                                  1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                     0; Gaps
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                                                                                                                                                                                                                                  Sequence 2, Application US/08460457
Patent No. 5719044
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shotegor, Oded
APPLICANT: Shotegor, Teai
APPLICANT: Goldstein, Marc A.
APPLICANT: Goldstein, Marc A.
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN FUSION PROTEINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.7%; Score 477; DB 1; Length 162; Best Local Similarity 97.8%; Pred. No. 3.8e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Pred. No. 3.8e-41;
tive 2; Mismatches 0;
                                                                                                                   61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                        66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNSYVDNTSKVTANFVKETASPISTYDTYLD 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Lesile
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7809-008
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 162 amino acida
TYPE: amino acid
Best Local Similarity 97.8
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-460-457-2
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US-08-460-458-2

RESULT 6

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GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
TITLE OF INVENTION: KITS AND METHODS OF DETECTION USING CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDCTQGQTFWCDHAGAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Pred. No. 3.8e-41;
2; Mismatches 0; Indels
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; Sequence 2, Application US/08460455
; Patent No. 5837914
; Patent No. 5837914
; Patent No. 5937914
; Patent No. 5937914
; APPLICANT: Shoseyov, Oded
; APPLICANT: Sholeyov, Oded
; APPLICANT: Sholeyov, Oded
; APPLICANT: Odolstein, Marc A.
; APPLICANT: Doi, Roy H.
; TILE OF INVENTION: CELLULOSE BINDING DOMAIN PROTEINS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,458
FILING DATE: concurrently herewith
CLASSIFICATION: 435
PFILING DATE: 14-APR-1993
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
APPLICATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,780-007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
Sequence 2, Application US/08460458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.8%;
Matches 90; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 162 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-460-458-2
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                                                                                                                                                                                                    ADDA.
STREET: 115.
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: U.S.A.
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REFERENCE/DOCKET NUMBER: 7809-005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: GELULOSE BINDING DOWAIN
NUMBER OF SEQUENCES: 33
CORRESSED: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: DATE : PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/330,394A
FRING APPLICATION NUMBER: US/08/330,394A
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,455
FILING DATE: CONCURTENTLY herewith
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REBREBNCE/COCKET NUMBER: 18,872
REBREBNCE/COCKET NUMBER: 18,872
REBREBNCE/COCKET NUMBER: 18,97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08330394A
Patent No. 5856201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.8<sup>†</sup>
Matches 90; Conservative
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6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
                                                                                                                                                                                                                                                                                                                          Gaps
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Patent No. 6005092

GENERAL INFORMATION:
APPLICANT: Shosey, Oded
TITLE OF INVENTION:
TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Score 477; DB 3; Length 163; 97.8%; Pred. No. 3.8e-41; Artive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Query Match 35.7%; Score 477; DB 2; Length 162; Best Local Similarity 97.8%; Pred. No. 3.8e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGNSYVDNTSKVTANFVKETASPISTYDDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,636
FILING DATE:
CLASSTET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7809-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BALGAIN, GETAIdine F.
REFERENCE/DOCKET NUMBER: 7809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
TELECOMMUNICATION INFORMATION:
TELEPHAN: (212) 790-9090
TELEX: 66441 PENNIE
TELEX: 66444 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 110-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.7
Best Local Similarity 97.8
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-006-636-7
                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-330-394A-2
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1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 477; DB 4; Length 163; Best Local Similarity 97.8%; Pred. No. 3.8e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08330394A
Patent No. 5856201
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yosef, Karmey
APPLICANT: Shpiegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Discussion of the Control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
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TITLE OF INVENTION: ARABIDOPSIS THALIANA TITLE OF INVENTION: GLUCANASE GENE, PROW NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 09/006,636
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-019
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FRAESEN, DOS
SOFTWARE: FRAESEN VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/325,274
FILING DATE:
                                                                                                                                                                                                                               STATE: N. COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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US-08-330-394A-29
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      MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                           7 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 66
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                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09006632
Patent No. 618440
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shani, Ziv
APPLICANT: Shani, Ziv
TITLE OF INVENTION: TRANSCENIC PLANTS OF ALTERED
TITLE OF INVENTION: MORPHOLOGY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                     61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                      61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-018
TELECHMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 1003-271
ZIP: 1003-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTERO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09325274
Patent No. 6323023
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INPORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACHERISTICS:
LENGTH: 163 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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US-09-325-274-7
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Gaps

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ARABIDOPSIS THALIANA ENDO-1,4-BETA-GLUCANASE GENE, PROMOTER AND PROTEIN
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1 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yeda Research and Development Co. Ltd.
APPLICANT: Ramot University Authority for Applied
APPLICANT: Research and Industrial Development Ltd.
APPLICANT: Technion Research and Development Foundation Ltd.
APPLICANT: Technion Research and Development Foundation Ltd.
APPLICANT: Willohe, Meir
APPLICANT: Willohek, Meir
APPLICANT: Lamed, Raphael
APPLICANT: Shoham, Yuval
TITLE OF INVENTION: MODIFIED CELLULOSE-BINDING DOMAIN (CBD)
TITLE OF INVENTION: PROTEINS AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 472; DB 2;
Pred. No. 1.2e-40;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GNSYVDNISKVTANFVKETASPISTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNSYVDNTSKVTANFVKETASPTSTYDTYVE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application PC/TUS9513813 GENERAL INFORMATION:
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NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: BAYE:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
TELERA: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
| TELEFAX: (2.12) 869-8864
| TELEX: 66441 PENNIE
| TELEX: 66441 PENNIE
| INFORMATION FOR SEQ ID NO: 22:
| SEQUENCE CHARACTERISTICS:
| TENED TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.8%;
Matches 89; Conservative
                                                                                                                                                                                                           : 156 amino acids amino acid
                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-330-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                TYPE: amir
TOPOLOGY:
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                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
FILING DATE: 27-OCT-1994
FILING DATE: 14-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 7809-005
TELLEFAX: (212) 799-9090
TELLEFAX: (212) 790-9090
TELLEFAX: (113) 864
TELLEFAX: (114) 864
TELLEFAX: (115) 864
TELLEFAX: (115) 864
TELLEFAX: (116) 864
TELLEFAX: (117) 860-864
TELLEFAX: (117) 860-864
TELLEFAX: (118) 860-864
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APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Shpiegl, Itai
APPLICANT: Shpiegl, Itai
APPLICANT: Obi, Roy H.
TITLE OF INVENTION: METHODS OF DETECTION USING THE
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%; Score 472; DB 2; L. 97.8%; Pred. No. 1.1e-40; tive 2; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GNSYVDNTSKVTANFVKETASPISTYDIYLD 92
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STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-330-394A-22,
; Sequence 22, Application US/08330394A
; Patent No. 5856201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC POS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.8°
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-330-394A-29
    MEDIUM TYPE:
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                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                       9 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGGKDGTFWCDHA-AI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                          4; Gaps
Query Match 18.4%; Score 245; DB 5; Length 167; Best Local Similarity 51.5%; Pred. No. 2.4e-17; Matches 53; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.4%; Score 245; DB 4; Length 476;
Best Local Similarity 51.5%; Pred. No. 1.1e-16;
Matches 53; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                              68 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 109
                                                                                                                                                                                                               61 LGN--SYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4. Application US/09339159B
Parent No. 6566114
GENERAL INFORMATION:
APPLICANT: Kauppinen, Markus
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Applicant, Markin
APPLICANT: Applicant, Mask
APPLICANT: Applicant, Mask
TITLE OF INVENTION: No. 6566114el Mannanases
FILE REFERENCE: 5440.204.US
CURRENT APPLICATION NUMBER: US/09/339,159B
CURRENT PILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Bacillus
US-09-339-159B-4
                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-339-159B-4
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318 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 376

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5, 2003, 20:16:47

Search completed: November Job time: 17.3592 secs

1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60

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TYPE: PRT ORGANISM: Piscirickettsia salmonis
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; NAME/KEY: SIGNAL
; LOCATION: (-95)..(-1)
US-10-261-446-6
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                                                                                                                                                                     November 5, 2003, 20:15:12 ; Search time 30.0656 Seconds (without alignments) 1462.395 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                          1335
1 MSVEFYNSNKSAQINSITPI......IYGTACPQPDGRWQVISTEK 256
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/ cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB_pep:**

/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US06_PUBCCMB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US06_PUBCCMB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:**

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/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:**

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/ cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:**

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/ cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:**

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/ cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:**

/ cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644079
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644079 segs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                              US-09-677-374-6
                        Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                Sequence:
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					SUMMARIES			
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Result		Query						
No.	Score	Match	Match Length DB	DB	ID	Description	c	
1	1335	100.0	256	12	US-10-261-446-6	Seguence 6,	1	Appl
7	832	62.3	161	12	US-10-261-446-4	Sequence		App]
m	815	61.0	162	12	US-10-261-446-2	Sequence	7	Appl
4	480.5	36.0	382	11	US-09-808-898-22	Sequence	22	Apr
ū	245	18.4	493	14	US-10-072-152-12	Sequence	12,	Apr
9	245	18.4	599	11	US-09-955-555A-29	Sequence	29	Apr
7	127.5	9.6	182	15	US-10-127-032-169	Sequence	165	169, Ar
ω	127.5	9.6	1352	11	US-09-784-554B-2	Sequence	ď	Appl
6	127	9.5	741	15	US-10-156-761-8100	Sequence		8100, 2
10	126.5	9.5	1350	11	US-09-784-554B-4	Sequence		Appl
11	123.5	9.3	1043	11	US-09-917-384-6	Sequence	9	Appl
12	123.5	9.3	1043	11	US-09-917-383-6	Sequence	é	App]
13	121	9.1	150	11	US-09-917-384-5	Sequence	'n	App]
14	121	9.1	150	11	US-09-917-383-5	Sequence	'n	Appl
15	121	9.1	1228	11	US-09-917-384-1	Sequence		App]

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Gaps

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100.0%; Score 1335; DB 12; Length 256; 100.0%; Pred. No. 1.4e-128; ive 0; Mismatches 0; Indels 0;

Matches 256; Conservative

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Query Match Best Local Similarity

9 9 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120

1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL

333-1 Sequence 1	5-400-1 Sequence 1, 5-400-6 Sequence 1,	5-400-5 Sequence 5, 5-400-4 Sequence 4,	-990-10 Sequence 10	8-19 Sequence 19,	95A-28 Sequence 28,	97-28 Sequence 28,	32A-28 Sequence 28,	89-28 Sequence 28,	08A-28 Sequence 28,	85A-28 Sequence 28, 91A-28 Sequence 28.	03A-28 Sequence 28,	64A-28 Seguence 28,	33A-28 Sequence 28,	15A-28 Sequence 28,	85A-28 Sequence 28.	23A-28 Sequence 28,	93A-28 Sequence 28,	-830A-28 Sequence 28,	-757A-28 Sequence 28,	187B-28 Sequence 28,	A-28 Sequence 2	75A-28 Sequence 28,	SINS								AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST	, AND ASSOCIATED PREVENIALIVE	46					
US-09-917- US-09-917-	10-15	US-10-15	-10-18	US-09-886-46	3C-09-97	US-09-978	566-60-SD	376-60-SU	US-09-978	376-60-SD	0S-09-978	US-09-978	366-60-SD	118-09-98	US-09-918	US-09-978	US-09-97	٩	-09	6-60-	S-09-9	US-09-97	ALIGNMENTS		1446) - -							CURRENT APPLICATION NUMBER: US/10/261,44	30	US 09/677,374	60/154,437		
###	121	12	12	10	0	2 5	200	11	# :	1:	11	11	::	1:	11	11	11	11	11	11	1	12			1026	26A1		Α.				1011	SD :	-60-	us 0			
1228	957	8 8 80 80	1621	922	285	285	285	285	282	285	285	285	282	262	285	285	285	285	282	285	285	282			ion IIS/	0301655		Kuzyk, Michael Burian Jan	Kav, William W	n, Julian	VACCINES AND	KICNE 6-64094	NUMBER	: 2002		UMBER:	1999-09	SEQ ID NOS: 20
4.00		ສ ໝ ນ ເນ	•						•			•	•	•				6.9	•	6.9	6.9	6.0	·		n] i cat	. us20	ATION:	zyk, m urian	av. Wi	Thornton,	NTION:	E. 461	CATION	G DATE	TION N	TION N	DATE:	SEQ ID NOS: 20
121	115	114	113	98	92	2 6	8 2	92	6 6	2 6	92	92	8 6	, , , ,	2 6	92	92	92	92	92	92	92		9	7-440-0	Publication No. US20030165526A1		¥		CANT: T	TITLE OF INVENTION: VACCINES	OF INVE	NT APPLI	CURRENT FILING DATE: 2002-09	APPLICATION NUMBER: US		FILING DATE: 1999-09	
116	166	21	22	2 6	25	97	28	53	30	32	33	34	32	9 6	. 89	3.6	40	41	42		44	45		RESULT 1	0-044-107-01-co	Publica	GENERA	APPLICANT:	APPLICANT:	APPLICANT:	TITLE	2117	CURRE	CURRE	PRIOR	PRIOR	PRIOR	NUMBER OF

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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, William
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING 1
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: SOURCE: 24729-128
CURRENT APPLICATION NUMBER: 08/091
PRIOR PILING DATE: 1099-03-15
PRIOR PELING DATE: 1099-03-26
PRIOR APPLICATION NUMBER: 08/777,716
PRIOR APPLICATION NUMBER: 08/777,716
PRIOR APPLICATION NUMBER: 08/777,716
PRIOR APPLICATION NUMBER: 08/777,716
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR PILING DATE: 11996-02-06
PRIOR PILING DATE: 11997-08-08
PRIOR PILING DATE: 11997-08-08
PRIOR PILING DATE: 11997-08-08
PRIOR PILING DATE: 11997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSVEFYNSNKSAQINSITPIIKIINISDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
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                                                                                                                                                                                                                                                                                                                                          Score 815; DB 12; Length 162;
Pred. No. 1.5e-75;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                               ; ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 22, Application US/09808898; Publication No. US20030092098A1
                                                                                                                                                                                                                                                                                                                                             Query Match
61.0%;
Best Local Similarity 98.8%;
Matches 158; Conservative 1
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Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                        LENGTH: 162
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                                                                                                                                                                                                                                   TYPE: PRT
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APPLICANT: BUTIAN, JAN
APPLICANT: KAY, William W.
APPLICANT: KAY, William W.
APPLICANT: KAY, William W.
APPLICANT: True or invention: Vaccines And Agents for inducing immunity in fish against Title of invention: Vaccines And Associated preventative Therapy Title of invention: Vaccines And Associated Preventative Therapy CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT PRILING DATE: 2002-09-30
FRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: Ruzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: AVA, William W.
APPLICANT: Thornton, Juliam C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-46194
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
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                                                                                                                            121 ROEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
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  181 EKVKAGOVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                           RQBVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                                                                              181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10261446
Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
                                                                                                                                                                                                                                                                                                                            241 ACPQPDGRWQVISTEK 256
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US-10-261-446-2
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APPLICANT: Bangera, M. Gital
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
TITLE OF INVENTION: BEFREENCE:
TITLE OF INVENTION: BIOPLIM FORMATION
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2001-04-19
PRIOR PELLING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGN--SYVDNTSKYTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 245; DB 11;
51.5%; Pred. No. 2.9e-16;
iive 16; Mismatches 30;
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FILE REFERENCE: GC278-C3
CURRENT APPLICATION NUMBER: US/09/955,555A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 08/559,958
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-10-17
PRIOR FILING DATE: 1995-10-17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 169, Application US/10127032; Publication No. US20030113742A1; GENERAL INFORMATION: APPLICANT: Whiteley, Marvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09784554B Publication No. US20030032162A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Clostridium thermocellum US-09-955-555A-29
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 51.5;
Matches 53; Conservative
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                61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS 120
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                                                                              118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162
                                                                                                                                              ---IGGAKVLGTAPGS 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bjornvad, Mads E.
APPLICANT: Glad, Sanne O. S.
APPLICANT: Glad, Sanne O. S.
APPLICANT: Glad, Sanne O. S.
APPLICANT: Schnorr, Markus S.
APPLICANT: Schnorr, Kirk
APPLICANT: Schnorr, Kirk
APPLICANT: Kongebak, Lars
TITLE OF INVENTION: No. US20020142438Alel Pectate Lyases
TITLE OF INVENTION: No. US2002007
TITLE OF INVENTION: No. US2002007
CURRENT APPLICATION NUMBER: US/10/072,152
CURRENT FILING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: 1344/97
PRIOR FILING DATE: 1997-11-24
PRIOR PRILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PRILING DATE: 1997-12-02
PRIOR PILING DATE: 1997-12-02
PRIOR PILING DATE: 1998-12-02
PRIOR PILING DATE: 1998-12-02
PRIOR PILING DATE: 1998-12-02
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-01-02
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Publication No. US20030027298A1
GENERAL INFORMATION:
APPLICANT: Bott, Richard R.
APPLICANT: Fowler, Timothy
APPLICANT: Fowler, Timothy
APPLICANT: Liu, Chung-Cheng
APPLICANT: Mard, Michael
APPLICANT: Xia, Hall-Ying
APPLICANT: Xia, Hall-Ying
APPLICANT: Sia, Hall-Ying
APPLICANT: Siame
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                                                                                                                   ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/10072152
Publication No. US20020142438A1
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Lange, Niels E
Bjornvad, Mads E.
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andersen, Lene N. APPLICANT: Schulein, Martin
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US-09-955-555A-29
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Query Match
Best Local Similarity
Matches 29; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                            3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62
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                                                                                                                                                                                                                                                                                                                                                     9; Gaps
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                                                                                                                                                                                                                                                                                                   Query Match
9.6%; Score 127.5; DB 11; Length 1352;
Best Local Similarity 30.4%; Pred. No. 0.001;
Matches 28; Conservative 19; Mismatches 36; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SCSKLNGKLVKMEKAATGA-DYYLEVS 1285
               APPLICANT: Schulein, Martin
TITLE OF INVENTION: FAMILY 44 XYLOGLUCANASES
FILE REFERENCE: 10017, 200-US
CURRENT APPLICATION NUMBER: US/09/784,554B
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1352
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 NSYVDNTSKVTANFVKETASPTSTYDTYLDPS 94
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APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIUVKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION WHERE: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FLILING DATE: 2001-05-30 PRIOR FILLING DATE: 2001-08-20 PRIOR FILLING DATE: 2001-08-02 SEQ ID NOS: 15109 LENGTH: 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8100
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, Publication No. US20030032162A1
, GENERAL INFORMATION:
 APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                        ORGANISM: Paenibacillus polymyxa
  Jorgensen, Per Lina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-156-761-8100
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APPLICANT:
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Publication No. US20030096342A1
GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU
APPLICANT: ADNEY, WILLIAM S.
APPLICANT: VINZANT, TODE B.
APPLICANT: HIMMEL, MICHAEL B.
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
TITLE OF INVENTION: TELLULOLYTICUS
FILE REFERENCE: 40170.6US01
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                                                                                                                                                                                                                                                                                                                                      DB 11; Length 1350;
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                                                                                                                                                                                                                                                                                                                                    9.5%; Score 126.5; DB 31.5%; Pred. No. 0.0013; tive 19; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 NSYVDNTSKVTANFVKETASPTSTYDTYLDPS 94
APPLICANT: Schulein, Martin
TITLE OF INVENTION: FAMILY 44 XYLOGLUCANASES
TITLE REFERENCE: 10017.200-US
CURRENT APPLICATION NUMBER: US/09/784,554B
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 4
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CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 6
LENGTH: 1043
                                                                                                                                                                                                                                                       ORGANISM: Paenibacillus polymyxa
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.3%; Score 123.5; DB 11; Length 1043;
Best Local Similarity 24.6%; Pred. No. 0.0019;
Matches 58; Conservative 28; Mismatches 79; Indels 71; Gaps
Sequence 6, Application US/09917383

Publication No. US20030104522A1

GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU
APPLICANT: DING, SHI-YOU
APPLICANT: VINZANT, TODD B.
APPLICANT: VINZANT, TODD B.
APPLICANT: HIMMEL, MICHAEL B.
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
TITLE OF INVENTION: CELLULOLYTICUS
FILE REFERENCE: 40170, 60201
CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 6
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Sequence 5, Application US/09917384

Publication No. US20030096342A1

GENERAL INFORMATION:

APPLICANT: DING, SHI-YOU

APPLICANT: VINZANT, TODD B.

APPLICANT: VINZANT, TODD B.

APPLICANT: WINZANT TODD B.

TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION: CELLULACUCATICUS

FILE REFERENCE: 40170.6US01

CURRENT APPLICATION NUMBER: US/09/917,384

CURRENT FILING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 14
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OTHER INFORMATION: Description of Artificial Sequence: Segment of
CHER INFORMATION: GUXA
OUS-09-917-384-5
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1043
TYPE: PRT
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LENGTH: 150
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1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFW-CDHAGA 59
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| Publication No. US20030096342A1
| GENERAL INFORMATION:
| APPLICANT: DING, SHI-YOU
| APPLICANT: DING, STILLIAM S. |
| APPLICANT: DING, STEPHEN R. |
| APPLICANT: HIMMEL, MICHAEL E. |
| TITLE OF INVENTION: CELLULOLYTICUS |
| TITLE OF INVENTION: CELLULOLOLYTICUS |
| TITLE OF INVENTION: LAWREN APPLICATION OF THE APPLICANT APPLICANT APPLICATION OF THE APPLICANT APP
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APPLICANT: DING, WILLIAM S.

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: TOOD B.

APPLICANT: TOO BECKER, STEBHER R.

TITLE OF INVENTION: THERNAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION: THERNAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION THERNAL TOLERANT

CURRENT APPLICATION NUMBER: US/09/917,383

CURRENT PILLING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 14

TYPE: PRT
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OTHER INFORMATION: GuxA
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                                                                                             12;
    Length 150;
                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                               60 LLGNSYVDNTSKVTANFVKETASP-TSTYDTYLDPSHMRGCL 100
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9.1%; Score 121; DB 11;
32.4%; Pred. No. 0.00021;
live 19; Mismatches 38;
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; Publication No. US20030104522A1
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Query Match
Best Local Similarity 32.4*
Matches 33; Conservative
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GenCore version 5.1.6
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5, 2003, 20:10:11; Search time 18.1278 Seconds (without alignments) 1358.089 Million cell updates/sec November Run on:

score: Title: Perfect #

US-09-677-374-6 1335 1 MSVEPYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cellulose-binding	rickettsial common			17K surface antige		17K antigen precur		_	scaffolding protei	probably celluloso	endoglucanase I (E	thermoactive cellu	- Cald		cellulase (EC 3.2.	mannan endo-1,4-be	1,4-beta-glucanase	cellulase (EC 3.2.	conserved hypothet	hypothetical prote	cellulase (EC 3.2.	17K surface antige		cellulase (EC 3.2.	outer membrane lip	hypol	cellulase homolog	cellulase (EC 3.2.
SUMMARIES	ID	A44140	D33971	B33971	A33971	G97860	C33971	A25972	PC6006	S36859	T30433	C97012	A47704	S12021	T31085	A43802	802711	A48954	T31337	T17120	D83169	F87413	G69593	AI3418	JN0111	A27198	S23787	B83514	A41897	A26874
	DB	7	~	7	~	N	~	7	7	~	N	~	7	~	7	7	~	~	~	7	~	~	N	N	~	~	N	~	~	7
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æ	Query	36.5	Н	21.3	н	21.3	20.7	20.7	18.7	18.4	17.5	16.7	14.1	14.1	11.3	11.0	10.7	10.7	10.6	10.4	9.6	9.1	9.1	9.0	8.6	8.5	8.4	8.4	8.3	8.5
	Score	487	288	285	285	285	276.5	276	249	245	233.5	223.5	188.5	188	151.5	147	143.5	143.5	142	138.5	127.5	122	121	120.5	115	113.5	112.5	111.5	111	109.5
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outer membrane lip	probable secreted	hypothetical prote	conserved hypothet	lipa protein [impo	probable lipoprote	lipA protein [impo	bifunctional cellu	outer membrane lip	outer membrane lip	probable outer mem	probable outer mem	lipA protein - Rhi	outer membrane pro	cellulase (EC 3.2.	PAL cross-reacting
AI0693	AE0644	G87629	B82837	AD2696	AF0289	D97478	140548	AG0443	C64921	F90922	B85771	558234	AD3350	S54744	164130
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155	179	232	257	142	155	125	486	155	155	155	155	139	232	504	155
8.2	8.2	8.2	8.2	8.1	8.1	8.0	8.0	8.0	7.8	7.8	7.8	7.8	7.7	7.7	7.6
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cellulose-binding protein A precursor - Clostridium cellulovorans C;Species: Clostridium cellulovorans C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 15-Oct-1999

C;Accession: A44140
R;Shoseyov, O.; Takaqi, M.; Goldstein, M.A.; Doi, R.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3483-3487, 1992.
A;Title: Primary sequence analysis of Clostridium cellulovorans cellulose binding protest A;Reference number: A44140, MUID:92228810; PMID:1565642
A;Accession: A44140
A;Accession: A44140
A;Accession: A44140
A;Residues: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-1848 cSHO>
C;Genetics:

A; Gene: cbpA

Gaps 90; Query Match

36.5%; Score 487; DB 2; Length 1848;
Best Local Similarity 46.8%; Pred. No. 6.7e-32;
Matches 116; Conservative 12; Mismatches 30; Indels 9

7;

92 33 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL S g 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120 ઠે

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121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180 125 ò g 181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238 144 -----GRITKSDWSNYTQTNDYSPDASSSTPVVNP-------KVTGYIGGAK--VL 185 ò 셤

GTACPOPD 246 239

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GTA-PGPD 192 186

RESULT

rickettsial common antigen precursor - Rickettsia prowazekii
N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833
C;Species: Rickettsia prowazekii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000
C;Accession: D33971; B71645
B;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989

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C;Accession: G97860
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-159 «KUR»
A,Cross-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish C,Species: Rickettsia conorii
C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residuss: 1-159 <AND>
C;Crosa-references: BB:M28480; NID:g152457; PIDN:AAA26376.1; PID:g152458
C;Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels

    Rickettsia rickettsii

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                                                                                                                                                                                                                                                                                                                                                                                                        21.3%; Score 285; DB 2; ilarity 37.9%; Pred. No. 1.9e-16; Conservative 31; Mismatches 53;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                 A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-159 < AND
A; Residues: 1-150 < AND
A; Cross-references: GB:M28482; NID:g152461
A; Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the R; Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A; Reference number: A71630; MUID:99039499; PMID:9823893
A; Retrence number: A71630; MUID:99039499; PMID:9823893
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-159 < AND
A; Residues: 1-159 < AND
A; Residues: 1-159 < AND
A; Experimental source: strain Madrid B
C; Genetics:
A; Gene: omp; RP833
C; Superfamily: rickettsial common antigen
C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201
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C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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Best Local Similarity
Matches 61; Conserv
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A;Residues: 1-1615,1617-1854 <GE2>
A;Cross-references: EMBL:L08665
R;Fujino, T.; Beguin, P.; Aubert, J.P.
FEMS Microbiol. Lett. 94, 165-170, 1992
A;Title: Cloning of a Clostridium thermocellum DNA fragment encoding polypeptides that }
A;Reference number: S25767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S36859
A;Accession: S36859
A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Cross-references: EMBL:L08665
A;Cross-references: EMBL:L08665
A;Cross-references: EMBL:L08665
A;Cross-references: EMBL:L08665
A;Cross-references: EMBL:L08665
A;Teribe: Sequencing of a Clostridium thermocellum gene (cipA) encoding the cellulosomal
A;Reference number: S33527; MUID:93302508; PMID:8316083
   the scaffolding protein CipC of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CipA protein - Clostridium thermocellum NyAlternate names: probable cellulosome protein large chain SL NyAlternate names: probable cellulosome protein large chain SL C;Species: Clostridium thermocellum C;Date: 13.-Jan.-1995 #semember ocellum C;Date: 13.-Jan.-1995 #semember ocellum C;Accession: S36859; S33527; S25767; S28659; T18261 R;Gerngross, U.T.; Demain, A.L. submitted to the EMBL Data Library, January 1993 A;Reference number: S36859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVBFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Fil-27/Domain: signal sequence #status predicted <SIG>
Fil-27/Domain: signal sequence #status predicted
File-187/Domain: cellulose binding #status predicted <CBD>
File8-292/Domain: hydrophilic <HYL>
File8-293/Domain: hydrophobic <HYBI>
                                                                                  A;Molecule type: DNA
A;Residues: 1-586 <PAG>
A;Residues: 1-586 <PAG>
A;Cross-references: GB:U40345; NID:g1314291; PID:g1314292
A;Experimental source: ATCC 35319
C;Genetics:
A;Title: Interaction between the endoglucanase CelA and A;Reference number: PC6006; MUID:96218696; PMID:8636029 A;Accession: PC6006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 249; DB 2;
33.8%; Pred. No. 8.6e-13;
7ative 32; Mismatches 81;
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A;Reference number: S28659
A;Accession: S28659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 NFDQSNDWSYTAA-
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Best Local Similarity
Matches 72; Conserv
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C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
C;Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii.
A;Reference number: A25972, MuID:87222152; PMID:3108232
A;Accession: A25972
A;Accession: A25972
A;Residues: 1-159 <AND>
A;Residues: 1-159 <AND>
A;Cross-references: GB:MI6486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
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               C;Species: Rickettsia typhi
C;Date: 16-Mar-1990 #text_change 20-Aug-1999
C;Accession: C33971
C;Accession: C33971
C;Accession: C33971
J: Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative Sequence analysis of a genus-common rickettsial antigen gene. A;Title: Comparative Sequence analysis of a genus-common rickettsial antigen gene. A;Reference number: A33971; MUID:89359171; PMID:2768201
A;Reference number: A33971
A;Reference number: A33971
A;Residues: 1-159 <AND>
A;Residues: 1-159 <AND>
A;Residues: 1-159 <AND>
C;Superfamily: rickettsial common antigen
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C;Species: Clostridium cellulolyticum
C;Species: 17-Aug-1990 #sequence_revision 16-Aug-1996 #text_change 13-Nov-1998
C;Accession: PCG006
R;Pages, S.; Belaich, A.; Tardif, C.; Reverbel-Leroy, C.; Gaudin, C.; Belaich, J. Bacteriol. 178, 2279-2286, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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Best Local Similarity 37.3%; Pred. No. 1e-15;
Matches 60; Conservative 31; Mismatches 54; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 159;
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ickettsial common antigen precursor - Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 276.5; DB 2 39.6%; Pred. No. 9.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Mismatches
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Best Local Similarity 39.61
Matches 55; Conservative
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C;Accession: C97012
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
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CiSpedies: Clostridium thermocellum
CiSpedies: Clostridium thermocellum
CiSpedies: Clostridium thermocellum
CiDate: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
CiAccession: A47704
G.P. Davidson, K.; Laurie, J.I.; Huskisson, N.S.; Gilbert, H.J.
J. Gen. Miorchiol. 139, 307-316, 1993
A.Title: Gene sequence and properties of Cell, a family E endoglucanase from Clostridium
A;Reference number: A47704; MUID:93171873; PMID:8436949
A;Accession: A47704
A;Accession: A47704
A;Accession: A47704
A;Accession: A47704
A;Accession: Company in the company in 
                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1483 «KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78886.1; PID:g15023809; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DAGSŠLEVOCRVAKND-- 153
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 223.5; DB 2;
Pred. No. 3.4e-10;
----hes 49;
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14.1%; Score 188.5; DB 2
Best Local Similarity 28.4%; Pred. No. 1.4e-07;
Matches 59; Conservative 20; Mismatches 48
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EVG-------FGSGAG-TLDPGGSV---
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28.4%;
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A;Gene: CAC0910
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C;Species: Clostridium acetobutylicum
                      A;Residues: 1216-1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1768,'R',1770-1854
A;Cross-references: EMBL:X67406
R;Fujino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
                                                                                                                                                     celluloson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scaffolding protein - Clostridium josui
C;Species: Clostridium josui
C;Date: 22-oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30433
R;Kakiuchi, M.; Isui, A.; Suzuki, K.; Fujino, T.; Fujino, E.; Kimura, T.; Karita, S.; SaJ. Bacteriol. 180, 4303-4308, 1998
A;Title: Cloning and DNA sequencing of the genes encoding Clostridium josui scaffolding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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A; Accession: T30433
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: L1162 KAK>
A; Kross-references: EMBL:AB004845; NID:93445476; PIDN:BAA32429.1; PID:93445477
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDP--SHMRGCL-QGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 SGNNYMDVISKVSGTF-NEVSPAVINADHYLEVALSSDAGSLPAGGSIEIQIRFARNDWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFSRQEVGAATGAVVGGVAGQLFGKGS----GRVSMAIGGAVLGGLIGSKIGQSMDQQDK 173
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                                                                                                                                                     cluster encoding the
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                                                                                                                                                                                                                                                                                                                                                              .Cross-references: EMBL:X67506; NID:g296879; PID:g296880; PIDN:CAA47840.1
;Genetics:
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                                                                                                                                               A, Title: Organization of a Clostridium thermocellum gene
                                                                                                                                                                                                            Reference number: Z18847; MUID:93209931; PMID:8458832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 245; DB 2; ilarity 51.5%; Pred. No. 7.5e-12; Conservative 16; Mismatches 30;
                                                                                                                                                                            e.
A.Reference number: Z18847; MUID:93209931; PMID:8458
A.Recession: T18261
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1821-1854 <FU2>
A.Gross-references: EMBL:X67506; NID:g296879; PID:g'
C,Genetics:
A,Gene: cipA
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198 -KISPTSISAKQGQ 210
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Best Local Similarity
Matches 53; Conserv
Molecule type: DNA
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cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Caldocellum s
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A; Residues: 1-915 <SAU>
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                                                                                                                                               NyAlternate names: avicelase I
C;Species: Clostridium stercorarium
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S12021
R;Jauris, S.; Ruecknagel, K.P.; Schwarz, W.H.; Kratzsch, P.; Bronnenmeier, K.; Staudenba
Mol. Gen. Genet. 223, 258-267, 1990
A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoach. A;Reference number: S12021; MUID:91066838; PMID:2250652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yalanse - Caldicellulosiruptor sp.
C; Species: Caldicellulosiruptor sp.
C; Species: Caldicellulosiruptor sp.
C; Species: O2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C; Accession: T31085
K; Morris, D.D.; Gibbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P.L.
submitted to the EMBL Data Library, December 1997
A; Description: Family 10 and 11 xylanase genes from Caldicellulosiruptor sp. Rt69B.1.
A; Reference number: Z20972
A; Reference number: Z20972
A; Accession: T31085
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1779 < MOR>
A; Residues: 1-1779 < MOR>
A; Consereferences: EMBL: AF036924; NID: G2760905; PID: G2760909; PIDN: AAB95326.1
C; Genetics:
A; Note: xynC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.1%; Score 188; DB 2; Length 986;
Best Local Similarity 27.6%; Pred. No. 1.8e-07;
Matches 47; Conservative 29; Mismatches 58; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 FSR-----OEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGL 159
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                                                                                                     S12021 thermoactive cellulase - Clostridium stercorarium
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------WSNYNQSNDYSFKQACLRQR 868
                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S12021
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-986 <JAU>
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RESULT A43802

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Risaul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile "A;Tette: cenb." a gene coding for a bifunctional cellulase from the extreme thermophile "A;Recession: A43802 MUID:91136262; PMID:2126700
A;Accession: A43802
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X13602
C;Function:
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce A;Description: hydrolyse degradation
C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 QSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEI 237
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Caldocellum saccharolyticum
C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
C;Accession: A43802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKIINTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHA--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 147; DB 2; Length 915; 23.2%; Pred. No. 0.00042; tive 35; Mismatches 64; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 A-----SNVTFKFVK-LSSSVSGADYYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 ----EIGFKSG-----AGÓLOPGKDTGEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 5, 2003, 20:15:57 Job time : 19.1278 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2003, 20:06:36 ; Search time 10.1693 Seconds (without alignments) 1183.846 Million cell updates/sec Run on:

US-09-677-374-6 1335 1 MSVEFYNSNKSAQTNSITPI.....IYGTACPQPDGRWQVISTEK 256 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score	ď	& Query March	Length	80	SUMMARIES	Description	ion
				3 :		211111111111111111111111111111111111111	
487 36.5	9		1848	-		_	clostridium
21	н.		129	н.	17KD_RICPR	4	rickettsia
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20	0		159	-	17KD_RICTY		rickettsia
8	0		154	Н	17KD_RICAU		rickettsia
13	o,		154	Н	17KD_RICPA	• •	rickettsia
13	σ		154	-	17KD_RICRH	• • •	rickettsia
13	σ		154	-	17KD_RICMO		rickettsia
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18.4	8.4		1853	Н	CIPA_CLOTM		clostridium
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14	14.1		986	Н	GUNZ_CLOSR		clostridium
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15 8	9.8		499	-1	GUN3_BACSU	_	bacillus su
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Φ	8.2		499	-	GUN1_BACSU		bacillus su
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7.	7.8		155	-	SLYB_ECOLI	_	escherichia
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7.	•		155	Н	PCP HAEIN		haemophilus
7.	٠		505	7	GUNV ERWCA	Q47096 e	erwinia car
7.	٠		700	~	GUNA_PAELA	-	paenibacill
	•		179	-	YCFJ_ECOLI	_	escherichia
7.	7.5		444	~	GUNN ERWCA	Q59394 e	erwinia car
7.	7.3		922	-	PMP1_CHLPN		chlamydia p

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                                                                          143
 LGNSYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                               181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY
                                                                                                               : | | :
----KVTGYIGGAK--VL
                                              121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                      ------KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                               genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson S.G.E., Zomorodipour A., Andersson J.O., Schbritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ215273; CAA15258.1; -.
PIR; D33971; D33971; PROKAR LIPOPROTEIN; 1.
OUTET Membrane; Lipoprotein; Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 159 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBABLE)
159 AA; 16672 MW; A33D404B65EEB071 CRC64;
                                                                                                                     ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP---
             (Rel. 19, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Madrid E;
MEDLINE=895917; PubMed=2768201;
Anderson B.B., Tzianabos T.;
"Comparative sequence analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 171:5199-5201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Madrid E;
MEDLINE-99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28482; AAA26378.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                         17 kDa surface antigen precursor.
                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                             GTACPQPD 246
                                                                                                                                                                    GTA-PGPD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
• Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondria.
                                                                                                                                                                                                                               17KD RICPR
P16624;
                                                                                                                                                                    186
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SEQUENCE
 61
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                ---IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                               103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Clin. Microbiol. 33:487-489(1995).
                                                                                                                                          Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
"Specific amplification of Rickettsia japonica DNA from clinical
specimens by PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 159;

      EMBL; D16515; BAA03965.1; -.

      PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

      Outer membrane; Lipoprotein; Antigen; Signal.

      SIGNAL
      1

      19
      BY SIMILARITY

      CHAIN
      20

      LIPID
      20

      SEQUENCE
      1554 MW; CDDCE7CEBDCD6B41 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.4%; Score 286; DB 1; Length 159, 37.9%; Pred. No. 5.8e-17; ive 32; Mismatches 52; Indels
                                                                                                                                                                                                                                                        213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 KOERROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         Z
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequen
01-NOV-1997 (Rel. 35, Last annota
17 kDa surface antigen precursor.
                                                                                                          GGLIGSKIGQSMDQQDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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ID 17KD RICJA
AC Q52764;
                                                                                                             157
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RESULT 4 17KD_RICCN

9

Gaps

16;

52; Indels

32; Mismatches

Conservative

21.6%; Score 288; DB 1; Length 159; 37.9%; Pred. No. 3.9e-17;

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153 1
159 AA;
                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia typhi
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=R.rickettsii;
MEDLINE=87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu Z., Bellini W.J.;
"Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
rickettsii.";
                                                                                                                                                                                                                                                                                                                                                                              *Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 170:4493-4500(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=R.conorii; STRAIN=Malish 7; MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A25972; A25972.

PIR; A31836; A31836.

PIR; A31971; A33971.

PIR; B31971; B33971.

PIR; B31971; B31971.

PIR; B97860; G97860.

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=1139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii: transcription and posttranslational
                                                                                                                                                 Rickettsia conorii, and
Rickettsia rickettsii.
Bacternia, Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsia.
NCBI_TaxID=781, 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
                                       01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  159 AA
                                                                                                                                                                                                                                                                                                           SPECIES=R.conorii, and R.rickettsii; MEDLINE=89359171; PubMed=2768201;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J03371; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 171:5199-5201 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 169:2385-2390(1987)
                                                                                                       17 kDa surface antigen precursor
OMP OR RC1287.
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EMBL; M28400; AAA26376.1; -
EMBL; AE008675; AAL03825.1; -
EMBL; M16486; AAA26381.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Anderson B.E., Tzianabos
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anchor (Probable).
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17KD RICCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 140
                                                                                                                                                                                                                                                              103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY--- 119
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                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson B.E., Tzianabos T.; "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps

    Bacteriol. 171:5199-5201(1989).
    SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
anchor (Probable).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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                                                                                                                           21.3%; Score 285; DB 1; Length 159; 37.9%; Pred. No. 7e-17; tive 31; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-ACYL DIGLYCERIDE (PROBABLE).
146 N -> D (IN REF. 3).
153 G -> E (IN REF. 3).
16581 MW; 206A2BBF74FCE169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane; Lipoprotein; Antigen; Signal. SIGNAL
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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PIR; C33971; C33971.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89359171; PubMed=2768201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Conservative
                                                                                                                                                                                                61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GAVLGGQİGAGMDEQDRRLABLTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=33992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Or send d...

EMBL; U17008; AAA82040.1; -.

EMBL; U17008; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 20 >154 17 kba SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 259; DB 1; Length 154; 36.5%; Pred. No. 9.8e-15;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
OUTER membrane; Lipoprotein; Antigen; Signal.
SIGNAL BY SIMILARITY.
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                                                  STRAIN=Maculatum;
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P50931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; m/10/46; Arracojj..., PROGRAT. LIPOPROTEIN; 1.
PROSITE; PSOGO13; PROKAR. LIPOPROTEIN; 1.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 kDa SURFACE ANTIGEN.
LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.1%; Score 268; DB 1; Length 154; 37.8%; Pred. No. 1.7e-15; ive 29; Mismatches 52; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA; 15967 MW; E3AA833346FAC320 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kba surface antigen precursor (Fragment).
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235 QEIYGTACPOPDGRWQVIS 253
                                                                         141 ÓTTÝGNÁCRÓPDGQWOVVN 159
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Conservative 2
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anchor (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia australis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia parkeri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=787;
                                                                                                                                                                                                                                                                                           17KD_RICAU
P50928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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P50930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GAVLGGQVGAGMDEQDRRIAELTSQKALETAPNGSNVFWRNFDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellulosomal scaffolding protein B (Cellulosomal glycoprotein S1/SL)
(Cellulose integrating protein B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MO 85-1084;
Stochard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridiaceae;
                                                                                                                                                                                                                                                                           Rickettsia amblyommii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; UIIULJ; AABU,'va..., PRORAE LIPOPROTEIN; 1.
PROSITE; PSOG013; PROKAE LIPOPROTEIN; 1.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 kDa SURFACE ANTIGEN.
I.TPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.1%; Score 255; DB 1; Length 154; 36.5%; Pred. No. 2.1e-14; ive 29; Mismatches 54; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AA; 15879 MW; E4FBE4C29D943581 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 KOERROOYCREFOOKAMIAGOKOEIYGTACPOPDGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |||||: | :||:|| || ||||||||120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              772 AA
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(Rel. 30, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U11013; AAB07704.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=33989;
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                                                                                                                                                                 01-OCT-1996 (
01-OCT-1996 (
01-OCT-1996 (
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01-OCT-1994
                                                                                                                         17KD RICAM
P50927;
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                                                                                                          17KD_RICAM
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                                                                                      RESULT 10
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                                                                                                                                                                                         SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                      64 GAVLGGOIGAGMDEODRRLAELTSORALETAPSGSNVEWRNPDNGNYGYITPNKTY---- 119
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                                                                                                                                                                                                                                                                               GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ohio 83-441;
Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia montana.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.2%; Score 256; DB 1; Length 154; 36.5%; Pred. No. 1.7e-14;
17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                       Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSOOJAT, PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

1 19 BY SIMILARITY.

CHAIN 20 >154 17 KDS SURFACE ANTIGEN.

LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE)
                                                                                                     ch
19.4%; Score 259; DB 1; Length 15.
l Similarity 36.5%; Pred. No. 9.8e-15;
57; Conservative 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
20 >154 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBAE
154 154 AA; 15895 MW; OCF85AD5D96DFEFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15881 MW; A09C53B8769E31DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 kDa surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U11017; AAB07705.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.2
Best Local Similarity 36.5
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anchor (Probable).
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20
154 1
154 AA;
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SEQUENCE
                   LIPID
NON TER
SEQUENCE
                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                           103
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Gaps

16;

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Cellulosomal scaffolding protein A precursor (Cellulosomal glycoprotein S1/SL) (Cellulose integrating protein A) (Cohesin)
                                     Clostridium thermocellum.
                                                                                                                                              Demain A.L.;
                                                                                                                                                                                homology."
                                                 Bacteria;
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                                                        Gilbert H.J.;

T "identification of the cellulose-binding domain of the cellulosome subunit S1 from Clostridium thermocellum YS.";

FEMS Microbiol. Lett. 78:181-186(192).

-!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME. IT PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE CELLULOSTIC ENZYMES PROBABLY THROUGH THE BINDING OF THE REPEATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS REPEATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS PRESENT IN CATALYTIC SOURCELL SUBRACE.

-!- SUBCELLULAR LOCATION: CELL SUBRACE.

-!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY THE CATALYTIC COMPONENTS OF THE CELLULOSOME.

-!- SIMILARITY: Contains at least 3 cohesin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%; Score 245; DB 1; Length 772; 51.5%; Pred. No. 9.2e-13;
                                                Poole D.M., Morag E., Lamed R., Bayer E.A., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGN -- SYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|: || || || || || || || || 340 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFIGGTLE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001947; CBD 37 1.
PROSITE; PS00018; BF HAND; UNKNOWN 1.
PROSITE; PS0448; CLOS CELLULOSOME RPT; 2.
Cellulose degradation; Cell wall; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BBF06DE5E094FE10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COHESIN 1.
LINKER (PRO/THR-RICH).
COHESIN 2.
LINKER (PRO/THR-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKER (PRO/THR-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELLULOSE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1853 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCKERIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCKERIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COHESIN 3
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001956; CBD 3.
InterPro; IPR002102; Cohesin.
InterPro; IPR002105; Dockerin 1.
InterPro; IPR002048; EP-hand.
Pfam; PP00942; CBM 3; 1.
Pfam; PP00963; Cohesin; 3.
Pfam; PP00404; Dockerin 1; 2.
                                  MEDLINE=93146373; PubMed=1490597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82491 MW;
                                                                                                                                                                                                                                                                                                                                  EMBL; X68233; CAA48312.1; -. HSSP; Q06851; INBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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461
607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIPA CLOTM
Q06851;
01-JUN-1994 (
01-NOV-1997 (
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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DOMAIN
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(Rel. 29, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=93209931; PubMed=8458832; Fujino T., Beguin F., Aubert J.-P.; Noganization of a Clostridium thermocellum gene cluster encoding the "Organization of a Clostridium thermocellum gene cluster encoding the cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface."; J. Bacteriol. 175:1891-1899(1993).
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Tavares G.A., Beguin P., Alzari P.M.;
"The crystal structure of a type I cohesin domain at 1.7-A
resolution.";
J. Mol. Biol. 273:701-713(1997).
-!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME. IT
PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CELLULOLYTIC ENZYMES.
-!- SUBCELLULAR LOCATION: CELL SURFACE.
-!- SUBCELLULAR LOCATION: CELL SURFACE.
-!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
THE CATALYTIC COMPONENTS OF THE CELLULOSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97238934; PubMed=9083107;
Shimon L.J.W., Bayer E.A., Morag E., Lamed R., Yaron S., Shoham Y.,
Frolow F.;
                                                                                                                                                                                                                                                                                                                                                                                                "Sequencing of a Clostridium thermocellum gene (cipA) encoding the cellulosomal SL-protein reveals an unusual degree of internal
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MEDLINE=97076134; PubMed=8918451;
TOXNO J., Lamed R., Chirino A.J., Morag E., Bayer E.A., Shoham Y.,
Steitz T.A.;
Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                 Gerngross U.T., Romaniec M.P.M., Kobayashi T., Huskisson N.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A cohesin domain from Clostridium thermocellum: the crystal
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Structure 5:381-390(1997).
                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 29-40 AND 42-43.
STRAIN=ATCC 27405 / DSM 1237;
MEDLINE=93302508; PubMed=8316083;
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EMBL; X67506; CAA47840.1; -.
PIR; S36859; S36859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .. Microbiol. 8:325-334(1993).
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SEQUENCE OF 1820-1853 FROM N.A.
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PDB; 1AOH; 08-JUL-98.

PDB; 1NBC; 26-SEP-96.

ILITE-FPO; IPR001956; CBD 3.

ILLE-PPO; IPR002102; Cohesin.
                                                                                          NCBI_TaxID=1515;
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                                                  CELLULOSE-BINDING (BY SIMILARITY).
CELLULOSE-BINDING (BY SIMILARITY).
LINKER (PRO/THR-RICH).
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COHESIN 6.
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COHESIN 9.
COHESIN 9.
DOCKERIN 1.
DOCKERIN 1.
DOCKERIN 1.
                                        CELLULOSOMAL SCAFFOLDING PROTEIN A.
COHESIN 1.
COHESIN 2.
InterPro; IPR002105; Dockerin 1.
InterPro; IPR002048; BP-hand.
Pfam; PP00942; CBM 3; 1.
Pfam; PF00942; CBM 3; 1.
Pfam; PF00404; Dockerin 1; 2.
Probom; PF004047; CBD 3; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00448; CLOS CELLULOSOME RPT; 2.
Cellulose degradation; Cell wall; Glycoprotein; Repeat; Signal; 3D-structure.
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369 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-A1 427
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STRAIN=NCIB 10682;
XX MEDIARE-93171873; PubMed=8436949;
A Hazlewood G.P., Davidson K., Laurie J.I., Huskisson N.S.,
Gilbert H.J.;
Gilbert H.
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Q02934;

Q1-FEB-1995 (Rel. 31, Last sequence update)

Q1-FEB-1995 (Rel. 31, Last sequence update)

Rel. 41, Last annotation update)

Endoglucanase I precursor (EC 3.2.1.4) (EGI) (Endo-1,4-beta-glucanase)

(Cellulase I).
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Clostridium thermocellum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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GUNI_CLOTM
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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

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------EVQIRFSKED 848
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01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotetion update)
Endoglucanase Z precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Thermoactive cellulase) (Avicelase I).
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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W; 35A60069A514A927 CRC64;
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InterPro: IPR001956; CBD 3.
InterPro: IPR001956; GBD 3.
InterPro: IPR001701; GIyCo_hydro_9.
Pfam; PF00759; GIyCo_hydro_9; 1.
ProDom; PD001947; CBD 3; 1.
PROSTIE; PS00599; GIYCOSYL_HYDROL_F9_1; 1.
PROSTIE; PS00699; GIYCOSYL_HYDROL_F9_2; 1.
Cellilose degradation; Hydrolase; Glycosidase; Signal.
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HSSP; P26221; 1TF4.
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Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGC--LQGSSLIIISVFLVGCAQN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
              linkages in cellulose, lichenin and cereal beta-D-glucans.
                                                                                                                                                                                                                                                  R HSSP; P26221; 1TF4.

R InterPro; IPR001956; CBD 3.

R InterPro; IPR0010101; GUP291.

R InterPro; IPR001701; GUP291.

R Pfam; PF00942; CBM 3; 2.

R Pfam; PF007442; DUF291; 2.

R Pfam; PF00759; GLYCOSYL HVDROL P9 1: 1.

R PROSITE; PS00699; GLYCOSYL HVDROL P9 1; 1.

R PROSITE; PS0699; GLYCOSYL HYDROL P9 1; 1.

R PROSITE; PS0699; GLYCOSYL HYDROL P9 1; 1.

R PROSITE; PS0699; GLYCOSYL HYDROL P9 1; 1.

R PROSITE; PS06991; GLYCOSYL HYDROL P9 1; 1.

R PROSITE; PS06991; GLYCOSYL HYDROL P9 1; 1.

R SIGNAL
                                            HYDROLASES). -- SIMILARITY: Contains 1 type-3 cellulose-binding (CBD) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OV-1997 (Rel. 35, Last annotation update)
Exoglucanase II precursor (EC 3.2.1.91) (Exocellobiohydrolase II)
(1,4-beta-cellobiohydrolase II) (Avicelase II).
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DOWAIN B.
DOWAIN B.
CELLULOSE-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Clostridium.
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; Pred. No. 6.7e-08;
29; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOGLUCANASE
                                                                                                                                                                                                                    EMBL; X55299; CAA39010.1; ALT_SEQ. PIR; S12021; S12021.
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27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             986 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A. STRAIN=NCIB 11754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1510;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 STRAIN=NCIB 11754;

MEDLINE=91364686; PubMed=1909625;

Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;

Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;

"Purification and properties of a novel type of

exo-1,4-beta-glucanase (avicelase II) from the cellulolytic

thermophile Clostridium stercorarium.";

Eur. J. Biochem. 200:379-385(1991).

-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
in cellulose and cellotetraose, releasing cellobiose from the non-
reducing ends of the chains.

-!- SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSF, Quesa; 1400.

InterPro; IPR001956; CBD 3.

InterPro; IPR001956; GBD 3.

InterPro; IPR001956; Glyco_hydro_48.

I Pram; PF00942; CBM 3; 1.

Pfam; PF02011; Glyco_hydro_48; 1.

PRIMTS; PR00844; GLHTDRLASE48.

R ProDom; PD011947; CBD 3; 1.

R ProDom; PD011903; Glyco_hydro_48; 1.

R ProDom; PD011903; Glyco_hydro_48; 1.

R ProDom; PD011903; Glyco_hydro_hydro_Hydrolase; Glycosidase; Signal.

SIGNAL 1 33 POTENTIAL.
                                                                                        Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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CHAIN 34 914 EXOGLUCANASE II.

SEQUENCE 914 AA; 103020 MW; DODB6017D6DFF82C CRC64;
Bronnenmeier K., Kundt K., Riedel K., Schwarz W.H., Staudenbauer W.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z69359; CAA93280.1; -. HSSP; O06851; 1NBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROLASES).
                                                                                                                                                                                 CHARACTERIZATION
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Search completed: November 5, 2003, 20:13:26 Job time : 11.1693 secs

63 NSYVDNTSKVTANFVKETASPTSTYDTYLD 92

3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62

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Q9774 clostridium Q1708 ricketteia Q17108 ricketteia Q1710 Getrivibrio Q913 clostridium Q4632 clostridium Q4632 clostridium Q5241 bacillu Q5241 caldicellul Q9255 caldicellul Q9255 caldicellul Q925 ricketteia Q91818 caldibacill Q9554 rhizobium l

Q8glu7 brucella su Q9hxi3 pseudomonas Q8vue8 brucella ab Q9a8m8 caulobacter Q93tj6 bacillus su Q931d0 bacillus su Q8yg27 brucella me

Q9rfx6 caldibacill

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97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuzyk M.A., Burian J., Thornton J.C., Kay W.W.;
"Identification of a genus-common Rickettsial surface antigen in the salmonid pathogen Pisciricketteia salmonis.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF184152; AAG17000.1; -.
SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piscirickettsia salmonis.
Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
Piscirickettslaceae; Piscirickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%; Score 815; DB 2; Length 162; 98.8%; Pred. No. 3.9e-60; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROOYCREFOOKAMIAGOKOEIYGTACROPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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1 MSVEFYNSNKSAQTNSITPI.....IYGTACPQPDGRWQVISTEK
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(c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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sp_fungi:*
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rickettsia

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108 53; Conservative
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK---IK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 235
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -.
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;
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Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H., Rickettsial relative associated with papaya bunchy top disease."; Curr. Microbiol. 36:80-84(1998).
EMBL, U76907; AAC02809.1; --
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Rickettsia felis (Rickettsia azadi).
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsiaee, Rickettsia.
NCBI_TaxID=42862;
                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA; 15050 MW; A7AFEEFDE0AEEE4C CRC64;
                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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40.1%; Pred. No. 1.3e-17;
ive 30; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98087556; Pubmed=9425244;
                                                                                                                                                                                                                                                               17 kDa common-antigen (Fragment).
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132 KAYGTACROPDGOWOVV 148
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                                                                                                PRELIMINARY;
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                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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Best Local Similarity
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AELTSQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIG 120
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"Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Schulenburg H.J.G.V.D., Majerus M.E.N.;
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"On the evolution of male-killing; Monophyletic origin and horizontal
transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
(Coleoptera: Coccinellidae).";
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269517; CAB96383.1; -.
EMBL; AJ269517; CAB96382.1; -.
NON TER 144 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 kDa antigen (Fragment).
Rickettsia cooleyi.
Bacternia, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsieae, Rickettsia.
NCBI TaxID=69410;
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male-killing Rickettsia from Adalia bipunctata.
Bacteria, Proteobacteria; Alphaproteobacteria; Rickettsiaees;
Rickettsiaceae; Rickettsiaee; Rickettsia.
NCBI_TaxID=38028;
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                                                                                                                                  137 AA; 14215 MW; A27597A9AFD85FC3 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                          KOERRQOYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVIS
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                            137 AA
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Matches

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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---1 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of scaffolding protein CipC and ORFXp, a new cohesin-containing protein in Clostridium cellulolyticum: comparison of various cohesin domains and subcellular localization of ORFXp."; J. Bacteriol. 181:1801-1810(1999).
                                                                                                                             MEDLINE=20575219; PubMed=11133455; Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Schulenburg H.J.G.V.D., Majerus M.E.N.; Incidence of male-killing Rickettsia Spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera: Coccinellidae)."; Appl. Braviron. Microbiol. 67:270-277(2001).

EMBL; AJZ69516; CAB96381.1; -. NON TER
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STRAIN=ARCC 35319;
Reverbel-Leroy C., Tardif C., Belaich A., Bernadac A., Gaudin C.,
Belaich J.;
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Interaction between the endoglucanase CelA and the scaffoldin protein CipC of the Clostridium cellulolyticum cellulosome."; J. Bacteriol. 178:2279-2286(1996).
                                                                                                                                                                                                                                                                                                                                                               Score 251.5; DB 2; Length 144;
Pred. No. 2.6e-13;
4; Mismatches 45; Indels 11.
           male-killing Rickettsia from Adalia decempunctata.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=120393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 35319;
MEDLINE=96218696; PubMed=8636029;
Bagges S., Belaich A., Tardif C., Reverbel-Leroy C., Gaudin
Belaich J.P.;
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STRAIN=ATCC 35319;
BEDLINE=299173902; PubMed=10074072;
Pages S., Belaich A., Fierobe H.P., Tardif C., Gaudin C.,
Belaich J.P.;
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144 AA; 14801 MW; C825472F16A56AE7 CRC64;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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39.4%; Pred. No. 2.v.
've 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     52; Conservative
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 17 kDa antigen (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                           76 TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 130
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                                                                                                                                   MEDLINE-99045882; PubMed-9828442; Stenos J., Roux V., Walker D., Raoult D.; Stenos J., Roux V., Walker D., Raoult D.; Stenos J., Roux V., Walker D., Raoult D.; Altickettsia honei sp. nov., the aetiological agent of Flinders Island spotted fever in Australia., Int. J. Syst. Bacteriol. 48:1399-1404(1998). EMBL; AP027124, ABB1846.1; -. EMBL; AF060706; AAD20231.1; -. EMBL; AF060704; AAD20231.1; -.
                                                                             Gaps
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Rickettsiaceae, Rickettsieae, Rickettsia.
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Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
14785 MW; C8254739CCA56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 137 AA; 14167 MW; 75BC1D0D745B428C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (17 kDa protein) (Fragment).
Rickettsia honei.
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Last sequence update)
Last annotation update)
                                 ch 18.9%; Score 252.5; DB 2; Il Similarity 39.4%; Pred. No. 2.1e-13; 52; Conservative 24; Mismatches 45;
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Q9K4W8;
01-0CT-2000 (TYEMBLER) 15,
01-0CT-2000 (TYEMBLER) 15,
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                                                                                                                                                                                                                                                                                                       131 OKAYGNACROPD 142
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                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
144 AA;
                                     Query Match
Best Local Similarity
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157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
               103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                    64 GAVLGGQIGAGMDEQDRRLAELISQRALETAPSGSNVEWRNPDNGSYGYVTPNKTYRNST 123
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                                                     MEDLINE=22182650, PubMed=12194779,
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 18.1%; Score 241.5; DB 2; Length 131; Best Local Similarity 39.1%; Pred. No. 1.5e-12; Matches 50; Conservative 24; Mismatches 43; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184232;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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EMBL; AJ427883; CAD20879.1; -.
NON TER 1 1
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SEQUENCE FROM N.A.
STRAIN=IrITA2;
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Pages S., Belaich A., Reverbel C., Tardif C., Fierobe H.P., Gaudin C., Bages S., Belaich A., Reverbel C., Tardif C., Fierobe H.P., Gaudin C., Bages S., Belaich D.;
Usubmitted (Or-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; U40345; AAC28899.2; -.
R HSSP; Q06812; NBC.
R InterPro; IPR001105; CBD 3.
R InterPro; IPR001105; CBD 3.
R InterPro; IPR001102; DUF291.
R InterPro; IPR005102; DUF291.
R Ffam; PF00942; CBM 3; 1.
R Ffam; PF00942; CBM 3; 1.
R ProDom; PD001947; CBD 3; 1.
R PRODOM; PD001947; CBD 3; 1.
R PRODOM; PD001947; CBD 3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD---PSHMRGCLQGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
"Molecular study and overexpression of the Clostridium cellulolyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Gaps
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MEDLINE=93084757; PubMed=1452660;
MEDLINE=93084757; PubMed=1452660;
MEDLINE=93084757; PubMed=1452660;
MEDLINE=931084757; PubMed=1452660;
MCDaracterization and comparison of Australian human spotted fever group rickettsiae.";
Group rickettsiae.";
J. Clin. Microbiol. 30:2896-2902(1992).
EMBL; M99391; AAA73386.1;
NON_TER 154 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia epp. ., . cum ubo (rragment).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Ricket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.7%; Score 249; DB 2; Length 1546; Best Local Similarity 33.8%; Pred. No. 9.4e-12; Matches 72; Conservative 32; Mismatches 81; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.3%; Score 244; DB 2; Length 154; llarity 35.3%; Pred. No. 1.2e-12; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 27 POTENTIAL.
28 1546 SCAFFOLDING PROTEIN.
1546 AA; 158748 MW; F8651504EC27809F CRC64;
                                  celCCF cellulase gene in Escherichia coli.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA; 15849 MW; F5C35855EDB439D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
(Clone PRB FISF 1), 5' end CDS (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 55; Conserva
                                                                                                                     SEQUENCE FROM N.A.
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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---1 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 SRQEVGAATGAVVGGVAGQLFCKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NKQGTGTILIGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rickettsial relative associated with male killing in the ladybird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Stouthamer R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.7%; Score 236.5; DB 2; Length 131; 38.3%; Pred. No. 4e-12; Live 24; Mismatches 44; Indels 11
                                          17 kDa protein (Pragment).
Rickettsia gp. California 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                          STRAIN=California 2;
Raoult D.;
"A new SFG rickettsia isolated from fleas ";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=California 2;
STRAIN=California 2;
SUBMILE (Recult D., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 131
131 AA; 13374 MW; 23C8819B29FFF860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 AA; 13344 MW; AIDCF71050DF52DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%; Score 236.5; DB 2; 38.3%; Pred. No. 4e-12; tive 24; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z
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MEDLINE=94117373; PubMed=8288533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beetle (Adalia bipunctata).";
J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 kDa antigen (Fragment).
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01-OCT-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 49; Conserv
                                                                                                                                                                                                                       NCBI_TaxID=147259;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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Q52637
    SO PRICE REPORTED TO THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---1 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TSQRALBAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.1%; Score 241.5; DB 2; Length 131; 1 Similarity 39.1%; Pred. No. 1.5e-12; 50; Conservative 24; Mismatches 43; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Protechacteria, Alphaprotechacteria, Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
rickettsiosis.";
Submitted (AIG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181036; AAG09427.1;
NON_TER 151 151
                                                                                                                                                                                                                                                                                                                                                                                                        13358 MW; D4152713C9FAA9CA CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein (Fragment).
Rickettsia helvetica.
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Last sequence update)
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                                                                                                                                                     Frico. Trom. From Lally."; Emerg. Infect. Dis. 8:983-986(2002). EMER.; AJ427882; CAD20878.1; -. NON TER 1 131 131 NON TER 131 131 NON TER 131 131 NON TER 131 NON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
MEDLINE=22182650; Pubmed=12194779;
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Q9F0Q1;
01-MAR-2001 (TEMBLrel. 16,
01-MAR-2001 (TEMBLrel. 16,
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Best Local Similarity
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RESULT 13 Q9F0Q1 ID Q9F0Q AC Q9F0Q DT 01-MADT 01-MA

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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSWDQQDK---I 174
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"First detection of spotted fever group rickettsiae in Ixodes ricinus from Italy.";
Energ. Infect. Dis. 8:983-986(2002).
EMBL; AJ427881; CAD20877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.6%; Score 235.5; DB 2; Length 131; Best Local Similarity 38.3%; Pred. No. 4.9e-12; Matches 49; Conservative 24; Mismatches 44; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=IrITA1;
MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=35789;
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                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                                     131 AA.
                                                                                                                                                                                                     PRT;
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                                                           235 QEIYGTAC 242
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                                                                                                124 OKAYGNAC 131
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SEQUENCE
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Search completed: November 5, 2003, 20:15:05 Job time: 38.582 secs

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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA41981.DAT:*
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| SIDSI/gcgdata/geneseqf_geneseqp_embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqf_geneseqp_embl/AA2002.DAT:*
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| SIDSI/gcgdata/geneseqf_geneseqp_embl/AA2003.DAT:*
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832
1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                Run on:
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			Description	Optimised OspA pro	Escherichia coli c	C17E2 OspA constru	E. coli codon opti	Piscirickettsia sa	OspA antigen amino	Piscirickettsia sa	Pseudomonas aerugi	OspA B-cell epitop
SUMMAKIES			ព	AAB81127	AAU97868	AAB81128	AAU97869	AAG78025	AAB81126	AAU97867	ABJ18820	AAB81130
			DB	22	23	22	23	22	22	23	24	22
			e Match Length DB ID	161	161	256	256	162	162	162	182	20
	dР	Query	Match	100.0	100.0	100.0	100.0	98.0	98.0	98.0	15.3	13.5
			Score	832	832	832	832	815	815	815	127.5	112
		Result	No.	-	7	m	4	ഹ	9	7	89	6

99CA-2281913 99CA-2281913

17-SEP-1999; 17-SEP-1999;

17-MAR-2001.

(KAYW/) KAY W W. (BURI/) BURIAN J. (KUZY/) KUZYK M A.

10		m	50	53	AAU97871	Outer surface lipo
7.		7	187	2 6	AAU1/565	M catarrnalls MCAI
17		2	422	7 6	AAB20105	2 2
41	-	າຕ	203	3 6	ABG80432	מים מים מים
15	1 -1	10	230	0 0	AAY34362	Porphorymonas ging
16		2	154	11	AAR05799	щ
17		12.1	155	23	ABG80423	
80 6		н (300	2 2	ABG15906	Novel human diagno
מיל כ		> c	147	7 0	AAB82611 ABB69847	Spider recombinant Droscophila melanog
2 6		o c	2309	4 6	ABB6533	Drosophila melanog
22		0	1251	7	ABB61254	Drosophila melanod
23		0	116	19	AAY11028	H. pylori ORF 01cp
24		0	423	22	AAB30695	A fusion of anti-C
25		6.6	71	24	ABP58756	Rickettsia rickett
26		9.0	112	53	ABP28121	Streptococcus poly
7.70		y 0	2017	7 6	ABG06301	Novel human diagno
0 0		, 0	196	2 5	ABF23639 ABB58019	Drogophila melanog
200		. 6	269	3 6	ABB90254	Himan polypentide
31		. 6	542	22	ABB65790	Drosophila melanog
32		9.7	542	22	ABB65791	Drosophila melanog
33		9.7	542	22	ABB70501	Drosophila melanog
34		9.6	82	23	ABP28119	Streptococcus poly
32		9.0	618	77	AAB56803	Human prostate can
36		9.0	1052	4, 0	AAE33//3	Human nucleic acid
ה מי מי		. 4	651	3 6	AA14009/	Spider Silv Proces
8		4.6	718	12	AAR14308	N.clavipes draglin
40		9.4	718	19	AAW53346	Nephila clavipes s
41	78.5	4.6	718	21	AAY59070	N. clavipes spider
42		4.0	240	24	ABP80680	ø 7
4.4		ט ט ט	120	4 0	AAM41343 ABD37981	Human GS930284 Dro
45		9.3	255	21	AAB11398	li expressio
					ALIGNMENTS	
RESULT 1	1 1 27					
	81127	standard;	, Protein;		161 AA.	
·	AAB81127;					
1	1-JUL-2001		(first entry)	<u> </u>		
-	Optimised O	OspA pr	protein 1	17E2	amino acid sequence.	
4 > 0 X & & & X	Poikilothermic vaccine; OspA; SRS.		fish, Piscirickettsi salmonid rickettsial	ciri rick	a salmonis; septicaemia	rickettsial pathogen; ; rickettsial disease;
	Piscirickettsia Synthetic.		salmonis			
	.ey	1	ocation	/Qua	lifiers	
	Region	- 1	109128 /label= B_cell_epit	а В	ll_epitope	
N N	CA2281913-A1	.;				

WPI; 2001-316844/34. N-PSDB; AAF86247.

Burian J,

кау мм,

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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsial salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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/label= C17E2_OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGCLÓGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
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                                                                                                                         Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 832; DB 23; Length 161; 100.0%; Pred. No. 3.6e-81; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Undefined_N-terminal_fusion_partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RROQYCREFQOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C17E2 OspA construct with N-terminal fusion partner.
              Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                Burian J,
                                                                                                                                                                                                                      Example 4; Fig 5; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 161; Conservative
                Kay WW,
                                                                                                                                                                              strain, as a vaccine
                                                              WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 AA;
                                                                                     N-PSDB; ABK52402
                   Thornton JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                               This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed 08pA, or an immunogenic fragment of ospA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen particularly polkilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 17E2. The DNA encoding ospA 17E2 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                              Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 832; DB 22;
100.0%; Pred. No. 3.6e-81;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli codon optimised OspA, 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97868 standard; Protein; 161 AA
                                                                                                                                                                                                                              Disclosure; Fig 5; 35pp; English
                          Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2000; 2000US-0677374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia salmonis
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Best Local Similarity Matches 161; Conserv

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Query Match

121

엄

AAU97868;

AAU97868 RESULT

161 AA;

Sequence

THORNTON J C. KAY W W. BURIAN J.

(THOR/) (KAYW/) (BURI/) (KUZY/) (

CA2339327-A1

Synthetic

15-MAR-2002.

KUZYK M A

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Gaps

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9

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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprocein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) with an N-terminal fusion used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGLIGSKIGGSMDQODKIKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                          Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 832; DB 23; Length 256; 100.0%; Pred. No. 6.6e-81; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                                Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG78025 standard; Protein; 162 AA
                                                                                                                                                                                                Burian J,
                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 5; 55pp; English.
                                         15-SEP-2000; 2000US-0677374.
19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piscirickettsia salmonis.
                                                                                                                                                                                              Kay WW,
                                                                                    THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                     strain, as a vaccine
                                                                                                                                                                                                                                         WPI; 2002-455221/49.
N-PSDB; ABK52403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 AA;
                                                                                                                                                  (KUZY/) KUZYK M A.
                                                                                                                                BURIAN J.
                                                                                                           KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200168865-A2
                                                                                                                                                                                                Thornton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                    (THOR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                (BURI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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$XXCCCCCCCCXXXXHHHXXBXBXBAAAAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a method for the protection against infection of a poikllothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of 0spA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli codon optimised OspA, 17e2 with N-terminal fusion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer surface lipoprotein, OspA, antibacterial, immunosupressive, vaccine, poikilothermic fish, fin-fish, Rickettsial septicaemia, Rickettisial disease, 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 832; DB 22; Length 256; 100.0%; Pred. No. 6.6e-81; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RRÓQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU97869 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 5; 35pp; English
                    99CA-2281913
                                                                99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100."
Matches 161, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia salmonis
                                                                                                                                                                                                                                            WPI; 2001-316844/34
                                                                                                                                                                                              Burian J,
                                                                                                                              BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA;
                                                                                                                                                                                                                                                                   N-PSDB; AAF86248
                    17-SEP-1999;
                                                                17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA2339327-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU97869;
                                                                                                       (KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                              Kay WW,
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ઠ 셤 ሯ 셤 ઠ XBXBXBXBXBXBX

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA, in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen in salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents p. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                            Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piscirickettsia salmonis outer surface lipoprotein OspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ROOYCREFQOKAMIAGOKQEIYGTACPOPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 22;
Pred. No. 2.4e-79;
1; Mismatches 1;
                                                                                                                                                                                                                                                           Example 2; Fig 2B; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU97867 standard; Protein; 162
                                                                                          Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-SEP-2000; 2000US-0677374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                                                             2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                          Burian J,
               (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody response
                                                                                                                                               N-PSDB; AAF86246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                        Кау WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGLIGSKIGOSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease, SRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                              New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                    Simard N, Brouwers H, Jones S, Griffiths S, Valenzuela P;
Burzio L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%; Score 815; DB 22; 98.8%; Pred. No. 2.4e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
110..129
/label= B cell_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OspA antigen amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB81126 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                                                            Claim 6; Fig 5; 25pp; English.
                                      2000GB-0005838.
2000GB-0016080.
2000GB-0016082.
2000GB-0018599.
                                                                                                                                 (AQUA-) AQUA HEALTH EURO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99CA-2281913
     12-MAR-2001; 2001WO-GB01055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.8°
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis.
                                                                                                                                                                                                                            WPI; 2001-639050/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 AA;
                                                                                                                                                                                                                                               N-PSDB; AAH79040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1999;
                                                                           01-JUL-2000;
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                                          11-MAR-2000;
                                                             01-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Region
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61 62 us-09-677-374-4.rag

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modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; and medical device-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                           compound capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGOSMDQQDKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poikilothermic fish, Piscirickettsia salmonis; rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease; SRS; antibody.
                                                                                                                                             Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 127.5; DB 24; Length 182; Pred. No. 1.8e-05; 13; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                           comprises a method for identifying a
                                         Greenberg EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 STVHDSSEKVVGYDVKYMLDGKAGOIRMERDP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 -KLNQSLEKV------KAGQVTRWRNP
                                                                                                                                                                                                                                   Claim 4; Page 152; 154pp; English.
                                         ŝ
                                            Lory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OspA B-cell epitope peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB81130 standard; Peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34...
Conservative
                                         ÄĞ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia salmonis.
(HARD ) HARVARD COLLEGE
                                            Bangera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316844/34.
                                                                                   WPI; 2003-075601/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                       N-PSDB; ABT14642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB81130;
                                         Whiteley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                  against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GGLIGSKIGQSMDQDDKIKLNQSLEKVKAGQVIRWRNPDTGNSYSVBPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic fibrosis, AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                 The invention describes a method of protecting a poikilothermic fish
                                                                                                                                                                 Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 23; Length 162;
Pred. No. 2.4e-79;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa biofilm formation-related protein #84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biofilm formation modulation; biofilm-associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ROQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                Kuzyk MA;
                                                                Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ18820 standard; Protein; 182
                                                                                                                                                                                                                                                       Claim 15; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.0%;
Best Local Similarity 98.8%;
Matches 158; Conservative
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24-OCT-2001; 2001US-344142P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                             Thornton JC, Kay WW,
                                                                                                                                                                                                                 strain, as a vaccine
                                                                                                       2002-455221/49
                   (KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA;
                                                                                                       WPI; 2002-455221/
N-PSDB; ABK52401.
(BURI/) BURIAN J.
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RESULT 8

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Sequence

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This invention relates to a method for the protection against infection of a poixllothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. Balmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen prickettsial septicaemia (SRS) and other rickettsial against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents an immunogenic epitope of the P. salmonis OspA protein. The peptide is used to raise rabbit anti-OspA antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial strain, as a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer surface lipoprotein, OspA, antibacterial, immunosupressive, vaccine, poikilothermic fish, fin-fish, Rickettsial septicaemia,
 vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                      13.5%; Score 112; DB 22; Length 20; 100.0%; Pred. No. 4.7e-05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer surface lipoprotein OspA based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian J, Kuzyk MA
                               Example 2; Page 17; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 17; 55pp; English.
                                                                                                                                                                                                                                                                                                                     109 PVRTYQRYNKQERRQQYCRE 128
                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97871 standard; Peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                          1 PVRTYQRYNKQERRQQYCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2000; 2000US-0677374.
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100."
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettisial disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUZYK M A
                                                                                                                                                                                                                              20 AA;
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                                                                                                                                                                                                                              Sequence
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(KUZY/)
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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of

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   to induce immunity
bacterial strain Piscirickettsia salmonis as a vaccine to induce immuni in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This sequence represents a synthetic peptide used to create polyclonal rabbit antibodies against the Piscirickettsia salmonis outer surface
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                Moraxella; vaccine; respiratory tract infection; antiinflammatory; auditory; antibacterial; otitis media; sinusitis; pneumonia.
                                                                                                                      ö
                                                                                                Length 20;
                                                                                                                   Indels
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                                                                                              13.5%; Score 112; DB 23; 100.0%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                             M catarrhalis MCA100414 protein SEQ ID NO: 10.
                                                                                                      100.0%; Prec. ...
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                                                                                                                                                                                                               AAO17565 standard; Protein; 197 AA
                                                                                                                                       109 PVRTYORYNKOERROOYCRE 128
                                                                                                                                                      PVRTYQRYNKQERRQQYCRE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradley B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-228742P.
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2000US-228438P.
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                                                                                                                                                                                                                                                         (first entry)
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                 Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loosmore S, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-401721/43.
N-PSDB; AAL46497.
                                                                                                        Local Similarity
                                                      lipoprotein, OspA.
                                                                          20 AA;
                                                                                                                                                                                                                                                                                                                                                       WO200218595-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000;
29-AUG-2000;
29-AUG-2000;
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29-AUG-2000;
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                                                                           Sequence
                                                                                                                                                                                                                                    AA017565;
                                                                                              Query Match
                                                                                                                   Matches
                                                                                                                                                                                           RESULT 11
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WO200262378-A2
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.
                                                                                                                                                                                The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce accines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVLLASSMALAGCANTGT --- TGNGTGFGGANVNKAVIGAVAGAL --- GGTAISKATGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adulte. The invention provides BASB113 polypeptides, and polymucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a
                   Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EKTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         media; pneumonia; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN
                                                                                                                                                                                                                                                                                                                                                                                                        Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Match 13.3%; Score 111; DB 23; I Local Similarity 33.3%; Pred. No. 0.0012; Nes 37; Conservative 15; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxella catarrhalis BASB113 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB20105 standard; Protein; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 67; 86pp; English.
                                                                                                                              Fig 9; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASB311; infection; otitis mantibacterial; antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-2000; 2000WO-EP05851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112458/12.
                                                                                                                                                                                                                                                                                                                                                   197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF30043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thonnard J;
                                                                                                                              Claim 28;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB20105;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperblebbing, Gram-negative bacterium, genetically modified, Tol gene peptidoglycan-binding, peptidoglycan-associated site, outer-membrane, bacterial infection, vesicle-shedding, Bleb, filter sterilised, detergent, deoxycholate, homogeneity, antibacterial, vaccine, TolQ, TolA, OmpCD, xOmpA, PAL-1, PAL-2.
                                                                                                                                                                                                                                                                                                    7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                                                                                          Gaps
polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least 1 antibody directed against a BASB113 polypeptide. BASB113 polypeptide also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                     ----AVLGGLIGSKIGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 103
                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 224;
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                                                                                                                                                                                                                            0.0014;
-hes 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thonnard
                                                                                                                                                                                                               ; Score 111; DB 22;
; Pred. No. 0.0014;
15; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis PAL-2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 71; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG80432 standard; Protein; 224
                                                                                                                                                                                                                 13.3%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2002; 2002WO-EP01361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001; 2001GB-0003171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                          37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berthet FJ, Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis.
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                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                          224 AA;
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Gaps

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activity with a vaccine mechanism of action. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease fundance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                                                            8 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG
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                                                                                                                              Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                     gingivalis; PG; periodontal disease; gingivitis;
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                                                                                                                                                       Indels
                                                                                                                               20;
                                                                                                                                                      31;
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                                                                                                                               Score 102.5; DB Pred. No. 0.011;
                                                                                (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 325-326; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               gingivalis protein PG3
                                                                                                                                                                                                                                                                                                             AAY34362 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hocking DN
Webb EA;
                                                                                                                               12.3%;
34.7%;
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98AU-0001546.
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(first entry)
                                                                                                                                                       25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas gingivalis.
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                                                                                                                                                                                                                            67 SKIGQSMDQQDK
                                                                                                                                                                                                                                           66 ALIGKKMDKQKK
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-385613/32
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine, antigenic
                                                                                                        223 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas
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                                                                                                                                                                                                                                                                                                                                                           20-MAR-2003
25-AUG-1999
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05-MAY-1998,
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                                                                                                                                                                                                                                                                                                                                     AAY34362;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agius
                                                                                                                                                       Matches
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                     the use of detergents such as deoxycholate, thus obviating chromatography purification and ultra centrifugation steps. Vesicles prepared from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present amino acid sequence represents a Moraxella catarrhalis protein, as described in the invention.
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         filter sterilised. The blebs can be made and harvested without
                                                                                                                                                                            7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          ----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 103
                                                                                                                                                                                                                                         |:|| :|| :|| :|| | EKTGRDAILGAAVGAAAGAYMERQAK---QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                    gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson MA;
                                                                                                                             Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphorymonas gingivalis peptides for preventing
                                                                                                                                                    35; Indels
                                                                                                                             DB 23;
                                                                                                                            13.3%; Score 111; DB 23 33.3%; Pred. No. 0.0014;
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                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Margetts
                                                                                                                                                                                                                                                                                                                                                                                            Porphorymonas gingivalis protein PG3
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                                                                                                                                                                                                                                                                                                           AAY34487 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hocking DM
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98AU-0003128.
98AU-0003338.
98AU-0003654.
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                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                    37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphorymonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-385613/32
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; antigenic
                                                                                                     224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX91705
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                                                                                                                                                                                                                                                                                                                                                                                                                    Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1998;
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25-AUG-1999
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10-MAR-1998
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23-APR-1998
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22-MAY-1998
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30-JUL-1998
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gingivitis
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                                                                                                      Sequence
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                                                                                                                             Query Match
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isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
(Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                230 AA;
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8888888888
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7; 8 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 66 15 ASVLAVALVFAGCGLN--NMAKGGLIGAGVGAIGAGVGNVAGNTAVGAIVGTAVGGAAG 72 Query Match 12.3%; Score 102.5; DB 20; Length 230; Best Local Similarity 34.7%; Pred. No. 0.012; Matches 25; Conservative 13; Mismatches 31; Indels 3; Gaps a ò

67 SKIGQSMDQQDK 78 : ||: ||: | 73 ALIGKKMDKQKK 84

ઠે ద Search completed: November 5, 2003, 20:12:50 Job time: 30.1969 secs

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Sequence 19701, Application US/09252991A

Sequence 19701, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
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  RESULT 1
US-09-252-991A-22817
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31960, A
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8009, Ap
28397, A
4442, Ap
26658, A
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Sequence 23334,
Sequence 31960,
Sequence 7802, P
                                                                                                                                                                                  5, 2003, 20:11:02; Search time 10.2884 Seconds (without alignments) 662.108 Million cell updates/sec
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832
1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-252-991A-2334
US-09-252-991A-31960
US-09-328-352-8009
US-09-328-352-8009
US-09-252-91A-28397
US-09-252-91A-2658
US-09-328-352-4442
US-09-328-352-4553
US-09-328-352-4553
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US-09-328-32S-6423
US-09-328-35S-6420
US-09-328-35S-6442
US-09-25S-991A-33036
US-09-25S-991A-33036
US-09-25S-991A-33036
US-09-328-32S-5755
US-09-328-32S-5755
US-09-328-32S-5755
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US-09-107-522A-4748
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Listing first 45 summaries

    protein search, using sw model

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Result

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Sequence 22817, Application US/09252991A

Sequence 22817, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: 107196, 136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22817
          Sequence 8, Appli
Sequence 19162, A
Sequence 31525, A
Sequence 26438, A
Sequence 2, Appli
Sequence 1100, A
Sequence 29681, A
Sequence 2681, A
Sequence 2681, A
Sequence 2681, A
Sequence 2841, A
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34.8%; Pred. No. 1.46-06;
          US-09-618-869-8

US-09-525-991A-19162

US-09-252-991A-31525

US-09-252-991A-30059

US-09-252-991A-30059

US-09-067-351-2

US-09-360-490-2

US-09-360-490-2

US-09-360-490-2

US-08-374-077C-2

US-08-374-077C-2

US-08-374-077C-2

US-08-378-35-7100

US-09-328-35-7100

US-09-328-35-7100

US-07-328-35-7100

US-09-252-991A-29681

US-09-107-532A-6584

US-09-252-991A-27975

US-09-252-991A-27975
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22817
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Best Local Similarity 34.84
Matches 32; Conservative
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Query Match
Best Local Similarity
Matches 23; Conserv
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,789
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ. ID NOS: 33142
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                                                                                                                                                                                                                                                                    Query Match
13.4%; Score 111.5; DB 4;
Best Local Similarity 25.7%; Pred. No. 7.4e-05;
Matches 35; Conservative 21; Mismatches 35;
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; Sequence 23334, Application US/09252991A
; Patent No. 6551795
; GENERAL INPORMATION:
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Best Local Similarity 24.1*
Matches 45; Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 19701
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US-09-252-991A-21754
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LENGTH: 306
                                                                                  LENGTH:
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APPLICANT: Marc J. Rubenfield et al.

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RESULT 6
US-09-328-352-7802
; Sequence 7802, Application US/09328352
; Sequence 7802, Application US/09328352
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
SEQUENCE SEQUENCE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MATC J. RUDEnfield et al.
APPLICANT: MATC J. RUDEnfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: US/00/094,190
PRIOR FILING DATE: US/00/094,190
NUMBER OF SEQ ID NOS: 33142
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Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.0%; Score 99.5; DB 4 Best Local Similarity 22.1%; Pred. No. 0.0052; Matches 38; Conservative 26; Mismatches 4
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US-09-252-991A-31960
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US-09-252-991A-23334
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4442
LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION AND ACTO SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPRENSICE: 107196.136 / 0918 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A PRIOR APPLICATION NUMBER: US/06/074,788 PRIOR APPLICATION NUMBER: US/06/074,788 PRIOR APPLICATION NUMBER: US/06/094,190 PRIOR FILING DATE: 1998-02-18 PRIOR PRIOR PRIOR DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                     7 GSSLIIISVFLVGCAQ-----AVVGGVAGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                        17;
                                                                                                                                    Score 86.5; DB 4; Length 127;
Pred. No. 0.034;
8; Mismatches 21; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 86.5; DB 4; Length 730; 22.0%; Pred. No. 0.36; tive 30; Mismatches 52; IndelB 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 WRNPDTGNSY-SVEPVRTYQRYNKQERRQQ 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4442, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Acinetobacter baumannii
US-09-328-352-4442
                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28397
                                                                                                                                      ch 10.4%;
1 Similarity 34.3%;
24; Conservative 8
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                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserv
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nes 33; Conserv
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SEQ ID NO 28397
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TYPE: PRT
                        LENGTH:
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Patent No. 6562958

PREMERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BUUGHIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BUUGHINI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8009
LENGTH: 126
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABGLGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                     87 PLILGWVQQQGGLQAALEKLKGAGLGSQVQSWVDPNQSN--SEVPTQQLQSLFNPADIEQ 144
                                                                                                                                                                                                                                                                                                                                                                                                         -----QDKIKLNQSLEKVK----AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQ 124
                                                                                                                                                                                                                                                                                                                                         8 SSLIIISVFLVGCAQNF--SRQEVGAATGAVVGGVAGQLFGKGSGR-VSMAIGGAV---- 60
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                                                                                                                                                                                                              11.1%; Score 92.5; DB 4; Length 199; 26.4%; Pred. No. 0.013; tive 19; Mismatches 45; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.8%; Score 90; DB 4; Length 126; Best Local Similarity 31.8%; Pred. No. 0.014; Matches 27; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                           34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQ-----
                                                                                                                                                                                                                                                              19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 YCREFQQKAMIAGQKQEIYG---TACPQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 VAQQAQ-----APKEQVYGAIASVLPQ 166
CURRENT APPLICATION NUMBER: US/09/328,352
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Acinetobacter baumannii
US-09-328-352-8009
                                                                                                                ; TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-7802
                   CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7802
                                                                                                                                                                                                            Query Match
Best Local Similarity 26.4*
Matches 39; Conservative
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Sequence 7.068, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: GARY L. Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION UNDERE: US/09/328,352

CURRENT APPLICATION UNDERE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 0.12;
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.0%; Score 83.5; DB 4; Length 84;
Best Local Similarity 42.5%; Pred. No. 0.043;
Matches 17; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGRAT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5149:
SEQUENCE CHARACTERLETICS:
LENGTH: 84 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...84
SEQUENCE DESCRIPTION: SEQ ID NO: 5149:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Sequence 6423, Application US/09328352; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Acinetobacter baumannii
US-09-328-352-6423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

9.9%;

Best Local Similarity 37.7%;

Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-107-532A-5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-328-352-7068
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US-09-328-352-6423
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US-09-320-352-4253
US-09-320-352-4253
Sequence 4.253, Application US/09328352
Pacquence 4.253, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPIJICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSGRVSMAIGGAVLGGLIGSKIGQSMDQ 75
                                                                                                                                                                                      21 AQNFSRQEVGAATGAVVGGVAGQLFGK----GSGRVSMAIGGAVLGGLIGSKIGQSMDQ 75
                                                                                        DB 4; Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 85; DB 4; Length 258 Best Local Similarity 29.7%; Pred. No. 0.13; Matches 22; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENČE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                       29;
                                                                                Query Match 10.3%; Score 86; DB 4; Best Local Similarity 34.8%; Pred. No. 0.64; Matches 24; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: 10-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5149, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 VGAATGAVVGGVAGQLFGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Acinetobacter baumannii
US-09-328-352-4253
               ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
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COUNTRY: USA
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925 RSSSTVNGS 933
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LENGTH: 258
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 -----RVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAG----QVTRWRNP 99
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9.9%; Score 82; DB 4; Length 215;
Best Local Similarity 23.9%; Pred. No. 0.22;
Matches 34; Conservative 22; Mismatches 48; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                        Query Match
9.9%; Score 82.5; DB 4; Length 217;
Best Local Similarity 25.2%; Pred. No. 0.2;
Matches 36; Conservative 20; Mismatches 52; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSG-
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DD------RYDRRYDRDRR 189
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; SEQ ID NO 7068
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6750
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November 5, 2003, 20:15:12; Search time 18.9085 Seconds (without alignments) 1462.395 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	٠,	7	Sequence 169, App	Sequence 16, Appl	8,	Sequence 8, Appli	Sequence 8, Appli	5,	Sequence 1381, Ap	Sequence 14378, A	Sequence 33055, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 88, Appl
SUMMARIES		TI OI	US-10-261-446-4	US-10-261-446-6	US-10-261-446-2	US-10-127-032-169	US-10-261-446-16	US/10/244	US/10/013	US/10/150	US-10-091-724-5	US-09-925-300-1381	US-10-156-761-14378	US-10-029-386-33055	US-09-861-597-1	US-10-414-760-1	US-10-244-821-88
	de	DB	12	12	12	15	12		15			10	15	12	σ	12	12
		Length	161	256	162	182	20	423	423	423	71	618	890	208	651	651	438
		Query Match	100.0	100.0	98.0	15.3	13.5	10.0	10.0	10.0	9.9	9.6	9.6	9.4	9.4	9.4	9.4
		Score	832	832	815	127.5	112	83	83	83	82.5	79.5	79.5	78.5	78.5	78.5	78
		Result No.	-	7	c	4	2	9	7	80	σ	10	11	12	13	14	15

Sequence 2107, Ap Sequence 28, Appl Sequence 28,	14444444
	09-978-188A-2 09-978-298A-2 10-143-031A-2 10-002-967A-2 10-017-083A-2 10-143-030A-2 10-187-749-4
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ALIGNMENTS

Sequence 4, Application US/10261446 Publication No. US20030165526A1 GENERAL INFORMATION:

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APPLICANT: RUZYK, Michael A.
APPLICANT: RUZYK, Michael A.
APPLICANT: RAY, William W.
APPLICANT: RAY, William W.
APPLICANT: RAY, William W.
APPLICANT: Thornton, Juliam C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
FRIOR APPLICATION NUMBER: US 69/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN OF SEION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 832; DB 12; Best Local Similarity 100.0%; Pred. No. 1.1e-79; Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-261-446-4
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
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APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Kay, William V.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISBASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVBPVRTYQRYNKQER 122
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                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                 3 RGCLQGSSLIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                    2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                   Gaps
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| JAPPLICANT: Whiteley, Marvin |
| APPLICANT: Bangera, M. Gita |
| APPLICANT: Bangera, M. Gita |
| APPLICANT: Large |
| APPLICANT: Greenberg, Severett Peter |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF |
| TITLE OF INVENTION: BIOFILM FORMATION |
| FILE REFERENCE: UIS-07010 NUMBER: US/10/127,032 |
| CURRENT APPLICATION NUMBER: US 60/285,190 |
| PRIOR APPLICATION NUMBER: US 60/285,190 |
| PRIOR APPLICATION NUMBER: US 60/344,142 |
| PRIOR APPLICATION NUMBER: US 60/344,142 |
| PRIOR SEQ ID NOS: 170 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| FORTION OF SEQ ID NOS: 170 |
| FORTION OF SEQ ID NOS: 170 |
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| FORTION OF SEQ ID NO
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                                                                                                                                               Length 162;
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                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 161
                                                                                                                                        Score 815; DB 12;
Pred. No. 6.8e-78;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 169, Application US/10127032; Publication No. US20030113742A1; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                        Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.8%
Matches 32; Conservative
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US-10-127-032-169
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                                                                                                                                                                                                                               Sequence 6, Application US/10261446

Publication No. US20030165526A1

GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Unlian C.
APPLICANT: Thornton, Unlian C.
APPLICANT: Thornton, Unlian C.
APPLICANT: Thornton, Unlian C.
APPLICANT: TOWNION: WACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
ITILE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
FILE REFERENCE: 4616-64094
CURRENT FILING DATE: 2002-09-30
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 6
LENGTH: 256
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Sequence 2, Application US/10261446

Publication No. US2003016526A1

GENERAL INFORMATION:

APPLICANT: Kuzyk, Michael A.

APPLICANT: Kuzyk, Michael A.

APPLICANT: Burian, Jan

APPLICANT: Thornton, Julian W.

APPLICANT: Thornton, Julian C.

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY

FILLE REFERENCE: 4616-64094

CURRENT APPLICATION NUMBER: US 99/677,374

PRIOR PLILNG DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/154,437

PRIOR FILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
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                                             121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 812; DB 12;
100.0%; Pred. No. 2e-79;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 161; Conservative
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LOCATION: (-95)..(-1)
US-10-261-446-6
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LENGTH: 162
121
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; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- genc
US/10/013,173-8
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US/10/150,762-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Graves, Scott S.
APPLICANT: Graves, Scott S.
APPLICANT: Graves, Scott S.
APPLICANT: Schultz, Joanne E.
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 690022.547C2
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.0%; Score 83; DB 15; Length 423; 1 Similarity 21.7%; Pred. No. 2.6; 33; Conservative 24; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.0%; Score 83; DB 15; Length 423; Best Local Similarity 21.7%; Pred. No. 2.6; Matches 33; Conservative 24; Mismatches 67; Indels
                        APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
APPLICANT: Reno, Jonh M.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILLE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILLING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 TFGAGTKLELKSSGSGSADPSKDSKAOVSAAE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AMIAGOKQEI----YGTACPOPDGRWQVISTE 160
       Schultz, Joanne Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10150762
Publication No. US20030103948A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gend
US/10/244,821-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQ----- 83
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10244821

Sequence 8, Application US/10244821

GENERAL INFORMATION:

APPLICANT: General:

APPLICANT: Graves, Scott Stoll

APPLICANT: Schultz, Joanne Elaine

APPLICANT: Schultz, Joanne Elaine

APPLICANT: Landerson, James Allen

APPLICANT: Banderson, James Allen

APPLICANT: Brack STREATHONE Exica A.

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: WETHODS OF USE THEREOF

CURRENT FILING DATE: 2002-09-16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 4.33
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10.0%; Score 83; DB 12; Length 423;
Best Local Similarity 21.7%; Pred. No. 2.6;
Matches 33; Conservative 24; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                          Query Match
13.5%; Score 112; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AMIAGOKOEI----YGTACPOPDGRWQVISTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 TFGAGTKLELKSSGSGSADPSKDSKAOVSAAE 278
; CURRENT FILING DATE: 2002-09-30; PRIOR APPLICATION NUMBER: US 09/677,374; PRIOR FILING DATE: 2000-09-15; PRIOR FILING DATE: 1999-09-17; NUMBER OF SEQ ID NOS: 20; SOFTWARE: Patentin version 3.0; SEQ ID NO 16; LENGTH: 20
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                      109 PVRTYQRYNKQBRRQQYCRE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10013173
Publication No. US20030095977A1
GENERAL INFORMATION:
APPLICANT: General Stephen C.
APPLICANT: Graves, Scott Stoll
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PVRTYORYNKOERROOYCRE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 US-10-261-446-16
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US/10/013
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Sequence 33055, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: HANZEL, DAVID K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: ABOMICA-X-2
             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1381
                                                                                                                                                                                                                                                                  76 dcredss----agyagicareassrkasyasssradsyadsradasyadsradasradasradasi
                                                                                                                                                                                                                                                                                                                                                                   132 GFGGGFGGGFGGGGGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKE 191
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                                                                                                                                                                                                                                                                                                                    55 AIGGAVLGGLIGSKIGQS---MDQQDKI-----KLNQSLEKVKA-----GQVTR
                                                                                                                                                                                                                  3 GCLQGSSLIIISVF--LVGCAQNFSRQEVGAAT--GAVVGGVAGQLFGKGS-GRVSM---
                                                                                                                                                                     Gaps
                                                                                                                                                                   Indels 33;
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                                                                                                                      Length 618;
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                                                                                                                                                                   54;
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                                                                                                                      DB 10;
                                                                                                                   Query Match
9.6%; Score 79.5; DE
Best Local Similarity 28.7%; Pred. No. 9.8;
Matches 41; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REPERROFE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                863 VAQG----GGONPAAIGEAIDAVERL 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 MAIGGAVLGGLIGSKIGQSMDQQDKI 79
                                                                                                                                                                                                                                                                                                                                                                                                                             WRNPDTGNSYSVEPVRTYQRYNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 WYEKH-GNSHQGEP-RDYSKYYK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14378, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Streptomyces avermitilis US-10-156-761-14378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-10-029-386-33055
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US-10-091-724-5
                                                                                                                                                                                                                                                                                                                      APPLICANT: Ashkar, Samy
TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
FILE REFERENCE: CMCC 820
CURRENT APPLICATION NUMBER: US/10/091,724
CURRENT FILING DATE: 2002-03-06
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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LOCATION: (524)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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191 GSSPKPWIYATSNLASGVPARFSGSGSGTSYSL----TISRVEAEDAATYYCQQWISNPP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 61
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Sequence 1381, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,
TITLE OF INVENTION: Uncleic Acide, Proteins and Antibodies
FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR PILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE PATENTIN VOICE: 2.00

SOFTWARE PATENTIN VOICE: 2.00
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                                                                                                                                                                                                                             Sequence 5, Application US/10091724
Publication No. US20030105310A1
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
                                                    133 AMIAGOKOEI ----YGTACPOPDGRWOVISTE 160
                                                                                                    247 TFGAGTKLELKSSGSGSADPSKDSKAQVSAAE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.9%; Score 82.5; DB Best Local Similarity 32.4%; Pred. No. 0.28; Matches 22; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (507)
OTHER INFORMATION: Xaa
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GAVLGGQI 71
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US-10-414-760-1
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APPLICANT: GARSON, Jean-Pierre
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERNATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGTVGLPQGVPGGGQDSTALKQTRRPAR 174
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78.5; DB 9; Length 651;
Pred. No. 13;
4; Mismatches 17; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                             INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                       Query Match 9.4%; Score 78.5; DB 12;
Best Local Similarity 30.8%; Pred. No. 3;
Matches 28; Conservative 12; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: MAP TO AC011553.3
OTHER INFORMATION: EXPRESSED IN HELA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10414760 Publication No. US20030192077A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09861597
Patent No. US20020064539A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.37
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ORGANISM: Nephila clavipes
                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-029-386-33055
                                                                            SEQ ID NO 33055
LENGTH: 208
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491 ÓGAGAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 651;
APPLICANT: Yang, Jianjun G.
TITLE OF INVENTION: Production of Silk-Like Proteins in Plants
FILE REFERENCE: BC1014 US NA
CURRENT APPLICATION WUMBER: US/10/414,760
CURRENT FILING DATE: 2003-04-16
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 438;
9;
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APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Brica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Indels
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9.4%; Score 78.5; DE
Best Local Similarity 35.3%; Pred. No. 13;
Matches 24; Conservative 4; Mismatches
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21.1%; Pred. No. 9;
Live 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 690022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 88, Application US/10244821; Publication No. US20030143233A1; GENERAL INFORMATION:
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ORGANISM: Nephila clavipes
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Best Local Similarity
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Search completed: November 5, 2003, 20:27:19 Job time : 18:9085 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                Copyright
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 protein search, using sw model OM protein November 5, 2003, 20:10:11; Search time 11.4007 Seconds (without alignments) 1358.089 Million cell updates/sec Run on:

US-09-677-374-4

832 1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	288	34.6	159	~	D33971	rickettsial common
7	285	34.3	159	N	B33971	Rickettsial common
m	285	34.3	159	~	A33971	Rickettsial common
4	285	34.3	159	~	G97860	17K surface antige
S	276.5	33.2	S	~	C33971	
ø	276	33.2	S	~	A25972	17K antigen precur
7	127.5	15.3	182	~	D83169	conserved hypothet
60	120.5	14.5	131	~	AI3418	17K surface antige
σ	112.5	13.5	155	~	S23787	outer membrane lip
10	111.5	13.4	154	~	B83514	conserved hypothet
11	109	13.1	179	~	AE0644	probable secreted
12	109	13.1	232	~	G87629	hypothetical prote
13	109	13.1	257	~	B82837	rved hyp
14	107.5	12.9	142	~	AD2696	lipA protein [impo
15	107.5	ς.	155	N	AF0289	ble lipo
16	101	12.9	125	7	D97478	lipA protein [impo
17	105.5	12.7	155	~	AI0693	outer membrane lip
18	104.5	12.6	155	~	C64921	nbran
19	104.5	12.6	155	~	F90922	d)
20	104.5		155	~	B85771	ar
21	104	12.5	139	7	S58234	lipA protein - Rhi
22	103	12.4	-	~	AG0443	outer membrane lip
23	103	12.4	232	0	AD3350	outer membrane pro
24	101	12.1	155	7	164130	eact
25	100.5	12.1	257	7	F87413	hypothetical prote
56	100		179	~	D85674	_
27	100	12.0	179	7	081	hetical pr
28	100	12.0	179	7	C64855	
29	99.5	12.0	304	7	H83636	hypothetical prote

132 2 D87353 179 2 ACC198 172 2 G91049 172 2 G91049 172 2 H65026 173 2 H65026 174 2 AB3091 175 2 AB3091 176 2 AB209 176 2 G97672 176 2 AB2097 176 2 AB2097 177 2 AB2097 177 2 AB2097 177 2 AB2097 177 2 AB2097 177 2 AB2097 177 2 AB2097 177 2 AB2097	hypothetical prote probable exported	probable lipoprote probable outer mem	probable outer mem hypothetical prote	hypothetical prote	hypothetical prote glycine-rich prote	porin [imported] -	hypothetical prote	conserved hypothet	probable tape meas	hypothetical prote	keratin, 54K type
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ALIGNMENTS

rickettsial common antigen precursor - Rickettsia prowazekii N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833

C;Species: Rickettsia prowazekii C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000 C;Accession: D33971; B71645 R;Anderson, B.E.; Trianabos, T. A;D Bacteriol. 171, 5199-5201, 1989 A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene. A;Reference number: A33971; MUID:89359171; PMID:2768201

A; Accession: D33971

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-159 cAND>
A;Cross-references: GB:M28482; NID:g152461
A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the A;Noters 30, 133-140, 1998
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893

A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A,Gene: omp, RPB33 C,Superfamily: rickettsial common antigen C,Keywords: surface antigen

Gaps 16; Length 159; 52; Indels Query Match

34.6%; Score 288; DB 2;
Best Local Similarity 37.9%; Pred. No. 1.6e-18;
Matches 61; Conservative 32; Mismatches 52.

9

63 61 8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL ઠે g

62 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117 δ

64 GAVLGGQIGASMDEQDRRILLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY---- 119

g

118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158 ઠે

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B33971 Rickettsial common antigen precursor - Rickettsia conorii

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141 QTTYGNACRQPDGQWQVVN 159
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Best Local Similarity
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C;Species: Rickettsia rickettsii
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C;Species: Rickettsia conorii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Accession: B:39: Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A31971; MUID:89359171; PMID:2768201
A;Recession: B33971
A;Accession: B33971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <AND
A;Residues: 1-159 <AND
A;Residues: GB:M28479; NID:g152463; PIDN:AAA26379.1; PID:g152464
C;Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch
     34.3%; Score 285; DB 2; Length 159;
1 Similarity 37.9%; Pred. No. 3e-18;
61; Conservative 31; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 KOERROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
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Best Local Similarity 37.9%; Pred. No. 3e-18;
Matches 61; Conservative 31; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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Matches
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C;Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
B. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii
A;Reference number: A25972; MUID:87222152; PMID:3108232
A;Accession: A25972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Anderson, B.E.; Tzianabos, T.
2. Bacteriol. 171, 5199-5201, 1989-64
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201
A,Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A,Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                          A;Accession: G97860
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 «KUR»
A;Cross-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SE TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsial common antigen precursor - Rickettsia typhi
C;Species: Rickettsia typhi
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Rickettsia rickettsii
C,Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 NKQGTGTLLGGAGGALLGSQFGHGKGQL-VGVGVGALLGAVLGGQIGASLDEQDRKLLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Rebidues: 1-159 cAND.
A;Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; PID:g152460
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 159;
                                                                                                                                                                                                                                                                                                                                                                     Length 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 -RNSTGQYCREXTQTVVIGGKQQKAYGNACRQPDGQMQVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.2%; Score 276.5; DB 2; Best Local Similarity 39.6%; Pred. No. 1.7e-17; Matches 55; Conservative 27; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                  34.3%; Score 285; DB 2; 37.9%; Pred. No. 3e-18; ative 31; Mismatches 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17K antigen precursor - Rickettsia rickettsii
                                                                                                                                                                                                                                                                          A,Gene: omp
C,Superfamily: rickettsial common antigen
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71

Gaps

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outer membrane lipoprotein precursor - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C;Accession: S21787
R;Baeumler, A.J.; Hantke, K.
B;Baeumler, A.J.; Hantke, K.
A;Title: A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Esc
A;Reference number: S23786; MUID:92121089; PMID:1732192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83514
R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.X.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Josep, S.; Olson, M.V.
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A,Reference number: A82950; MUID:20437337; PMID:10984043
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A;Molecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04442.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACPQPD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AVAIAAVTLIGCANNNILSGDVFSASQAKQVQTVIYGTLLSVRPVIIQGGDDNNVMGAIG
                                                                                                                                                                                                                                                                                                                                                                      14 GKGSGFPS--LGGSSQKPETNLLASLGNGLFGNSASQLSAADRRKALEAEYRALEYSPAG
                                                                                                                                                                                                                                                                                                         46 GKGSGRVSMAIGG-----AVLG-GLIGSKIGQ--SMDQQDKIKLN-QSLEKVKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <BAE>
A;Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                     Indels 23;
                                                                                                                                                                        DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                        14.5%; Score 120.5; DB 2;
31.7%; Pred. No. 0.0011;
ive 17; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 112.5; DB 2
; Pred. No. 0.0067;
19; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 -- NQSLEKVKAGQVTRWRNPDTGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 SLIIISVFLVGCAQN-----FSRQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%;
24.7%;
A; Experimental source: strain 16M
                                                                                                                                                                        Query Match
Best Local Similarity 31.7*
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
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                                                            A; Map position: I
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                                   C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: D83169 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-182 <STO> A;Coss-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07206.1; GSPDB:GN001 A;Residues: 1-182 <STO> A;Genetics: A;Gene: PA3819 C;Superfamily: PAL cross-reacting lipoprotein
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Cispecies: Brucella melitensis
Cispecies: Brucella melitensis
Cispecies: Brucella melitensis
Cistoria de la melitensis
Cistoria de la melitensis
Cistoria de la melitensis
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                 8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                Gaps
                                                                A;Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 127.5; DB 2; Length 182; 34.8%; Pred. No. 0.00037;
                                                                                                                                                                            Length 159;
                                                                                                                                                                        Query Match 33.2%; Score 276; DB 2; Length 15: Best Local Similarity 37.3%; Pred. No. 1.9e-17; Matches 60; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KAGOVTRWRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                   A; Residues: 1-159 <AND>
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Matches
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4

Gaps

99

---VGAAT 33

73

16;

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Conserved hypothetical protein XF0178 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B82837
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Rolander (27) cSIM>
A;Cross-references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN0011
A;Cross-references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN0011
A;Stmpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HI
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigri chado, M.A.; Madedira, A.M.B.N.; Madedira, A.M.B.N.; Madedira, A.M.; Matchins, E.C.; Franco, M.C.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak,
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair,
A;Reference number: A59328
A;Reference number: A59328
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                                 A;Accession: G87629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <STO>
A;Cross-references: GB:AE005673; NID:g13424723; PIDN:AAK25035.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2696
                                                                                                                                                                                                                                                                                                                                                                                                                         17 LVGCAQNFSRQEVGAATGAVVGGVAGQLFGK---GSGRVSMAIGGAVLGGLIGSKIGQSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                      13.1%; Score 109; DB 2; Length 232; 33.7%; Pred. No. 0.021; ive 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109; DB 2; Length 257; Pred. No. 0.024; 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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Best Local Similarity 47.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 DQQDKIKLNQS-
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                             32;
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                                                                                                                                                                                                                             A; Gene: CC3073
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: AE0644
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, F. Connetron, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
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Nature 6.; Moule, S.; O'Gaora, P.
Nature 6.; Moule, S.; O'Gaora, P.
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Nature 6.; Moule, S.; O'Gaora, P.
Nature 6.; Moule, S.; O'Gaora, P.
Nature 6.; Moule, S.; O'Gaora, P.
Nature 6.; Moule, S.; O'Gaora, P.
Nature 6.; Moule, S.; O'Gaora, P.; Pinn: CAD08336.1; PID: Gl6502381; GSPDB: GN00176
C; Ganetics:
A; Gene: STY1252
C; Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession. G87629
R;Accession. G87629
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon h. J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable secreted protein STY1252 [imported] - Salmonella enterica subsp. enterica serov C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #sequence_revision 09-Nov-2001
                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK 89
                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                             1 MRKSALİVASFTAMALALGGCQSSLTGDTYSREEARTVQTVRMGTIQALRPVKIEGTKTP
                                                                                                                                                                                                                                                                                                                                                                                                                             29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL-----
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein CC3073 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GSVLGAVAGGVIGHQFGGGRGKDVATVVGALGGGYAGNQIQGSMQESD-
                                                                                                                                                                    Length
                                                                                                                                                                                                                                    Indels
                                                                                                                                      Score 111.5; DB 2;
Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                5 LOGSSLIIIS----VFLVGC----AQNFSROE-
                                                                                                                                                                                                                                 21; Mismatches
                                 C'Genetics:
A;Gene: PA1053
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 STRAYVOQVDOĞQIFR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable secreted protein STY1252
C;Species: Salmonella enterica ent
      source: strain PA01
                                                                                                                                                                    13.4%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NQSLEKVKAGQVTR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 CPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 IPL-DGNGOLVLNNK 178
                                                                                                                                                                                                                             35; Conservative
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 35; Conserv
          A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
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probable lipoprotein slyB [imported] - Yersinia pestis (strain CO92)
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0289
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <KUR>
A;Residues: 1-155 <KUR>
A;Gonetics:
C;Genetics:
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2656
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Goserimental source: strain C58 (Dupont)
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: circular chromosome
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C;Superfamily: PAL cross-reacting lipoprotein
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5, 2003, 20:15:56

Search completed: November Job time: 11.4007 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2003, 20:06:36 ; Search time 6.39551 Seconds (without alignments) 1183.846 Million cell updates/sec Run on:

US-09-677-374-4 832 1 MRGCLQGSSLIIISVFLVGC.....IYGTACPQPDGRWQVISTEK 161 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	•	Description	rickettsi	rickettsi		P22882 rickettsia									P55741 escherichia		-	-			P45931 bacillus su	-	P37723 salmonella	escheri	Q00310 candida alb	P17853 salmonella			Q8z460 salmonella	Q9z158 rattus norv	plue	P26011 mus musculu		9 strep	P13645 homo sapien
SUMMARIES		ID	ᅜ	17KD_RICJA	17KD_RICCN	17KD_RICTY	17KD_RICAU	17KD_RICPA	17KD_RICRH	17KD_RICMO	17KD_RICAM	17KD_RICCA	PCP YEREN	SLYB_SALTY	SLYB_ECOLI	PCP_HABIN	YCFJ_ECOLI	YFGH_ECOLI	K1CJ BOVIN	XKDO_BACSU	YQBO_BACSU	YKR2_CAEEL	OSMB_SALTY	OSMB_ECOLI	KRE2_CANAL	CYSH_SALTY	NUS7_YEAST	Y615_AQUAE	CYSH SALTI	STXG_RAT	VP5_BTV11		CANS_BOVIN		K1CJ_HUMAN
		Length DB	-1			159 1					154 1	80 1	155 1	155 1	155 1	155 1	179 1	172 1	526 1	1332 1	1585 1	783 1	72 1	72 1	431 1	243 1	541 1	132 1	243 1		526 1	806 1	263 1	890 1	593 1
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		Score	288	286	285	276.5	268	259	259	256	255	156	112.5	105.5	104.5	101	100	95	90	90	88	87.5	86.5	85.5	84.5	82.5	82.5	82	81.5	81.5	81.5	80	79.5	•	79
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P37665 escherichia P19837 nephila cla P41167 thiobacillu P19482 bos taurus P46724 mycobacteri P2599 rattus norv P25705 homo eapien P06813 oryctolagus P19483 bos taurus Q03265 mus musculu P02535 mus musculu P46199 homo sapien
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2119 7119 3114 467 467 553 553 727 727
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## ALIGNMENTS

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B33971; B33971
G97860; G97860
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                    | ::||:: | | | :: : : | ||:| | | SKIMIIALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQL-VGVGVGALL
                                                                 GGLIGSKIGOSMDOODK----IKLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYORYN
                                                                                     SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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MEDLINE=95229950; PubMed=7714214;
MEDLINE=95229950; PubMed=7714214;
Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
Fariya Y., Katayama T., Yoshida Y., Kaiho I.;
Specimens by PCR.";
J. Clin. Microbiol. 33:487-489(1995).
-: SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Porteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiaceae, Rickettsiaceae, Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Or Send ....

EMBL: D16515; BAA03965.1; -.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 19 BY SIMILARITY.

CHAIN 20 159 17 kDa SURFACE ANTIGEN.

20 20 N-ACYL DIGLYCERIDE (PROBABLE).

**c=4 MW; CDDCE7CEBDCD6841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.4%; Score 286; DB 1; Length 159; 37.9%; Pred. No. 5.7e-18;
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                                                                                                                                  118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                   118 KOERROOYCREFQOKAMIAGOKOEIYGTACPOPDGRWOVIS 158
                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
17 Aba surface antigen precursor:
                                                                                                                                                                                                                                                      159 AA.
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                                                                                                                                                                                                                                                                                                                                                                     Rickettsia japonica
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RESULT 3 17KD_RICCN ID _17KD_RICCN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=R.rickettsii;
MEDLINE=87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu Z.Y., Bellini W.J.;
                                                                                                                                                                                                                                                                             "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 170:4493-4500(1988).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                  Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from
Rickettsia rickettsii: transcription and posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
                                                                                                                                    Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
N -> D (IN REF. 3).
            01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                        Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=781, 783;
                                                                                                                                                                                                                         SPECIES=R.conorii, and R.rickettsii;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=R.conorii; STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, J03371; -; NOT_ANNOTATED_CDS.
PIR; A25972; A25972.
PIR; A31836; A31836.
PIR; A33971; A33971.
                                              28-FEB-2003 (Rel. 41, Last annota
17 kDa surface antigen precursor.
OMP OR RC1287.
                                                                                                                                                                                                                                                                                                             Bacteriol. 171:5199-5201(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol, 169:2385-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M28479; AAA26379.1; -. EMBL; M28480; AAA26376.1; -.
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EMBL; M16486; AAA26381.1; -.
EMBL; J03371; -; NOT_ANNOTAT
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                                                                                                    Rickettsia conorii, and Rickettsia rickettsii.
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37.8%;
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                                                                                                                                                                                                                                                                                                                                   anchor (Probable).
                                                                                                                                                                                                Rickettsia australis.
                                                                                                                                                                                                                                                                                    Baird R.W., Ross B.,
Submitted (OCT-1991)
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Best Local Similarity
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SEQUENCE FROM N.A.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                   GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
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                                                                                                       8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFCKGSGRVSMAIG-GAVL 61
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                           34.3%; Score 285; DB 1; Length 159; 37.9%; Pred. No. 7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 159 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBABLE)
159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
 153 G -> E (IN REF. 3).
16581 MW; 206A2BBF74FCE169 CRC64;
                                                                                                                                                                                                                                           120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                            118 KOERROOYCREFQOKAMIAGOKQEIYGTACPOPDGRWQVIS 158
                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 276.5; DB 1; 39.6%; Pred. No. 3.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane; Lipoprotein; Antigen; Signal.
                                                                         31; Mismatches
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                            17 kDa surface antigen precursor.
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                                                                          61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anchor (Probable).
   153 1
159 AA;
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Best Local Similarity
                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia typhi
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 CONFLICT
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                                             Query Match
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Rickettsiaceae; Rickettsieae; Rickettsia.
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 268; DB 1; Length 154; 
; Pred. No. 2e-16; 
29; Mismatches 52; Indels 1
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01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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154 AA
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01-OCT-1996
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01-0CT-1996
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                                                                        SEQUENCE
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P50929;
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAVLGGOIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
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                                      Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELDULAR LOCATION: Attached to the outer membrane by a lipid
anchor (Probable).
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Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTIE; PSO00137, PROXAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

1 19 BY SINTLARITY.

CHAIN 20 >154 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.1%; Score 259; DB 1; Length 154; Best Local Similarity 36.5%; Pred. No. 1.2e-15; Matches 57; Conservative 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 154
154 AA; 15897 MW; 5D06F45F9DBD5EEC CRC64;
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Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 19 8 SIMILARITY.
CHAIN 20 >-154 17 kDa SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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01-OCT-1996
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SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                     64 GAVLGGQIGAGMDBQDRRLAELISQRALETAPSGSNVEWRNPDNGNYGYITPNKTY---- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ohio 83-441;
Stothard D.K., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
Submitted (DEC-1994) to the EMBI/GenBank/DDBJ databases.
Submitted (DEC-1994) to the trached to the outer membrane by a lipid
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                                                                                                          31.1%; Score 259; DB 1; Length 154;
36.5%; Pred. No. 1.2e-15;
iive 30; Mismatches 53; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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EMBL; U11017; AAB07705.1; -.

EMBL; U11017; AAB07705.1; -.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

Outer membrane; Lipoprotein; Antigen; Signal.

20 >154 17 kDa SURFACE ANTIGEN.

20 >154 17 kDa SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE)
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Pred. No. 2.2e-15;
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N-ACYL DIGLYCERIDE (PROBABLE)
                                                         154 AA; 15895 MW; OCF85AD5D96DFEFB CRC64;
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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36.5%;
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                                                                                                                                                                             57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anchor (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWR
               Azad A.F., Sacci J.B. Jr., Nelson W.M., Dasch G.A., Schmidtmann E.T., Carl M.; "Genetic characterization and transovarial transmission of a typhus-like rickettsia found in cat fleas."; Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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"A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli.";
J. Bacteriol. 174:1029-1035(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 AA; 8372 MW; AD289A48EAB19E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; M82879; -; NOT ANNOTATED CDS.
InterPro; IPR000437; Prok lipoprot.
PROSITE; PS00013; PROKAR LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 37, Last annotation update)
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STRAIN=ATCC 51872 / WA-C / Serotype O:8;
MEDLINE=92121089; PubMed=1732192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 156;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane lipoprotein pcp precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane; Lipoprotein; Antigen
NON_TER 1 1
NON_TER 80 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
  MEDLINE=92108069; PubMed=1729713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 NPDTGNSYSVEPVRTYQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 26, Created)
(Rel. 26, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NPDNGNYGYVTPSKTYK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. INFLUENZAE PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P31484;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR PCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SKIMIJALAASTLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Stothard D.R., Raiph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=33989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Or Bena.

EMBL; U11013; AAB07704.1; -.

EMBL; U11013; PROKAR LIPORROTEIN; 1.

PROSITE; PS00013; PROKAR LIPORROTEIN; 1.

SUCHAL 1 19 BY SIMILARITY.

SIGNAL 20 >154 17 kDa SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 KOERROOYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
30.6%; Score 255; DB 1;
Best Local Similarity 36.5%; Pred. No. 2.6e-15;
Matches 57; Conservative 29; Mismatches 54;
                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AA.
                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kDa surface antigen (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anchor (Probable).
                                                                                                                                                                                                                                                             Rickettsia amblyommii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MO 85-1084;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=788;
                                                                                                          17KD RICAM
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RESULT 10 17KD_RICCA ID 17KD_RICA AC P29697;

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                                                                                                                                                                                      -----VGAAT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S. typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; SPECIES S.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T., Connerton P.,
Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIESS typhimurium;
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                         51;
                                                                                                                              DB 1; Length 155;
                                                                   18 15 OUTER MEMBRANE LIPOPROTEIN PCP.
18 18 N-ACYL DIGLYCERIDE (POTENTIAL).
155 AA; 15362 MW; 8AD6BE2132E849FA CRC64;
                                                                                                                                                                                                                                             GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL
                                                                                                                                                         Indels
                                                                                                                             13.5%; Score 112.5; DB 1; 24.7%; Pred. No. 0.0053; tive 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein slyB precursor.
SLYB OR STM1445 OR STY1677 OR T1313.
                                                                                                                                                                                                                                                                                                                                                                                                        155 AA
                                                                                                                                                                                                                                                                                                      --NOSLEKVKAGQVTRWRNPDTGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                     | : :|: :| | 127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                       9 SLIIISVFLVGCAQN-----FSRQE----
           PIR; S23787; S23787.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal.
                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium, and Salmonella typhi.
 EMBL; X60448; CAA42977.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
                                                                                                                                         Best_Local Similarity 24.7
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                       SLYB SALTY
Q53549;
                                                                                                                                                                                                                                              34
                                                                                                    SEQUENCE
                                                                                                                              Query Match
                                                           SIGNAL
                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                         SLYB_SALTY
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 GOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IIISVFLVGCAQNFSRQEVGAATGAVVGGVA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644564; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18."; J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                       anchor (Potential).
-!- SIMILARITY: TO E.COLI SLYB, H.INFLUENZAE PCP AND Y.ENTEROCOLITICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                             J. Baccellular LOCATION: Attached to the outer membrane by a lipid
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008762; AAL20367.1; -
EMBL; AL627271; CAD01922.1; -
EMBL; AE046838; AA068963.1; -
EMBL; AE046889; AA068963.1; -
EMBL; AE046889; AA068963.1; -
EMBL; AE046889; AA0689698; AA068989; AA068989; AA06898718; AB00013; BROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal; Complete proteome.
SIGNAL 1 17 OUTER MEMBRANE LIPOPROTEIN SLYB.
LIPID 18 18 N-ACYL DIGLYCERIDE.
SEQUENCE 155 AA; 15548 MW; 82FDDCDCBABD55A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 105.5; DB 1; Length 155; 24.3%; Pred. No. 0.021; Live 20; Mismatches 53; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane lipoprocein slyB precursor.
SLYB OR B1641 OR Z2655 OR ECS2350 OR SF1668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GNTIMVVQKQGNTRFSAGQR 140
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SPECIES-E.coli;
MEDLINE-96133688; PubMed-8544813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 GNSYSVEPVRTYORYNKOER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELYB ECOLI STANDARD; F
P55741; P76183;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli,
Escherichia coli 0157:H7, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S80790; AAB35871.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSL-----
                              enterica serovar Typhi CT1
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MBDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli Colification of a netochemorrhagic Rocherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
-I- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
   Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin W., Wang J., Liu H., Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Xan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                             SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=E.coli; STRAIN=0157:H7 / BDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                         "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alba H., Baba T., Fullta K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=97251357; Pubmed=9097039;
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MEDLINE-88115138; PubMed=2828309;

MEDLINE-88115138; PubMed=2828309;

Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;

"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Heemophilus influenzae.";

J. Bacteriol. 170.489-498 (1988).
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STRAIN=Rd / KW20 / ATCC 51907;
MBDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Frasser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
PCP OR LPP OR HI1579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104.5; DB 1; Length 155; Pred. No. 0.026;
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                                                                             EMBL; AE000259; ANALYTIC...

EMBL; D90807; BAA15402.1; -..

REMBL; AE005387; AAG56630.1; -..

REMBL; AE015187; AAN43250.1; -..

REMBL; AE015187; AAN43250.1; -..

REMBL; B85771; B85771.

REMBL; P80922; F90922.

DR PROGENE; EG13409; BLyB.

DR PROSITE; P800013; PROKAR LIPOPROTEIN; 1.

POTENTIAL.

FOURTH MEMBLAND: Lipoprotein; Signal; Complete proteome.

AUCET membrane; Lipoprotein; Signal; Complete proteome.

AUCET MEMBLAND: AND AUCET MEMBLANDE LIPOPROTEIN SL
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155 AA; 15602 MW; 543EBBA4069A5FA3 CRC64;
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A -> T (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
                  entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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Matches 33; Conservative
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18
98
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                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  "Whole-genome random sequencing and assembly of Haemophilus influenzae
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MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ishemoto K., Inada T., Itoh T., Kajinara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
Man J. Horiuchi T.;
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SPECIES=E.COli, STRAIN=KI2 / MG1655;
MEDLINE=9726617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                    Rd.";
Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.1%; Score 101; DB 1; Length 155; 39.6%; Pred. No. 0.052;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                           -!- SIMILARITY: TO B.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; HI1579; -.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
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NCBI_TaxID=562, 217992, 623;
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EMBL; U32832; AAC23228.1; -.
PIR; 164130; 164130.
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Escherichia coli 06, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=E.coli; STRAIN=K12;
MEDLINE=81236546; PubMed=6265208;
Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.;
"Nucleotide sequence coding for the respiratory NADH dehydrogenase of Escherichia coli. UUG initiation codon.";
Eur. J. Biochem. 116:165-170(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang Y., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                               SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928; MEDLINE=22388234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud Mayhew G.E., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
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"Intrinsic and extrinsic approaches for detecting genes
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-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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EMBL; V00306; -; NOT ANNOTATED CDS.

EMBL; AE015138; AAN42732.1; ALT_INIT.

PIR; C64855; C64855.

EcoGene; EG12444; ycfJ.
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MEDLINE=95075659; PubMed=7984428;
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EMBL; D90746; BAA35925.1; -.
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29agc7 rickettsia

Q8vue8 brucella ab

08/927 brucella me 09/2189 rhizobium m 09/2181 pseudomonas 08/8016 pseudomonas 08/8016 pseudomonas 08/8019 garobacteri 08/8018 garobacteri 08/8018 garobacteri 09/228 garobacteri 09/228 garobacteri 09/228 garobacteri 09/228 garobacteri 08/228 garobacteri 08/228 garobacteri 08/228 garobacteri 08/228 garobacteri 08/228 farizobium 10/22854 rhizobium 10/2285

Scoring table:

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SURAIN=LF-89;
Kuzyk M.A., Burian J., Thornton J.C., Kay W.W.;
"Identification of a genus-common Rickettsial surface antigen in the salmonid pathogen Piscirickettsia salmonis.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
SEMBL, AF184152; AAG17000.1; -
SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
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Bacteria; Proteobacteria; Gammaprotec
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NCBI_TaxID=1238;
              Created)
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BELLINE-1217364; PubMed=11321078;
BOUYET D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98087556; PubMed=9425244;
MEDLINE=98087556; PubMed=9425244;
Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;
NRICKettsial relative associated with papaya bunchy top disease.";
Curr. Microbiol. 36:80-84(1998).
EMBL: U76907; AAC02809.1;
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                                                                                                                                                                                                                                                                                          9.
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Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=789;
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NCBI_TaxID=42862;
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.int. J. Syst. Evol. Microbiol, 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -
SEQUENCE 159 AA; 16497 MW; 34CSB020AF470A1F CRC64;
                                                                                                                                                                                                                                                 148 AA; 15050 MW; A7AFEEFDEOAEEE4C CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                   Query Match 36.5%; Score 303.5; DB 2; Best Local Similarity 40.1%; Pred. No. 1.1e-19; Matches 55; Conservative 30; Mismatches 43;
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Rickettsia felis (Rickettsia azadi).
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                                                                                                                                                                                                                                                                                                                                                                                                                    KAYGTACRQPDGQWQVV 148
                                                                                                                                                                                                                                                                                                                                                                                                        141 EIYGTACPQPDGRWQVI 157
                                                      01-001-2002 (TrEMBLrel. 06, 17 kDa common-art
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                       148
                                                                                                      Rickettsia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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79 --IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ONFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.8; Score 258.5; DB 2; Length 137; Local Similarity 39.3%; Pred. No. 1.1e-15; nes 53; Conservative 25; Mismatches 46; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17kDA antigen (17 kDa antigen) (Fragment).
male-killing Rickettesia from Adalia bipunctata.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae, Rickettsiaes, Rickettsia.
                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsiaceae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 137 AA; 14215 MW; A27597A9AFD85FC3 CRC64;
                                                                       118 KQERRQQYCREFQQXAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                       17 kDa antigen (Fragment).
Rickettsia cooleyi.
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DB 2; Length 144;

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80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
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                                                                                                                                                                                 MEDLINE=20575219; PubMed=11133455;
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria)
the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera:
Coccinellidae).";
           male-killing Rickettsia from Adalia decempunctata.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=120393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AA; 14801 MW; C825472F16A56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.2%; Score 251.5; DB 2; 39.4%; Pred. No. 5.2e-15; ive 24; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                          Appl. Environ. Microbiol. 67:270-277 (2001)
EMBL, AJ269516; CAB96381.1; ...
NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
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17 kDa antigen (Fragment)
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                                                                                                                                                                                                                                                                                                                                   76 TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 130
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MEDLINE=99045882; PubMed=9828442;

MEDLINE=99045882; PubMed=9828442;

Stenos J., Roux V., Walker D., Raoult D.;

Rickettsia honei sp. nov., the aetiological agent of Flinders Island spotted fever in Australia.";

Int. J. Syst. Bacteriol. 48:1399-1404(1998).

EMBL; AF027124; AAB1846.1; -.

EMBL; AF060706; AAD20231.1; -.
                                                                                                                                                                                                25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
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                                                                                                           11;
                                                       Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia honei.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
144 AA; 14785 MW; C8254739CCA56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 AA; 14167 MW; 75BC1D0D745B428C CRC64;
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39.4%; Pred. No. 4.9e-15;
:ive 24; Mismatches 45;
                                                                                                              24; Mismatches 45;
                                                    30.3%; Score 252.5; DB 2 39.4%; Pred. No. 4.2e-15;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
17 kDa antigen (17 kDa protein) (Fragment).
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Best Local Similarity 39.4%
Matches 52; Conservative
                                                                                                              52; Conservative
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                                                       Query Match
Best Local Similarity
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Q9K4W8;
01-OCT-2000 (
01-OCT-2000 (
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Q9K4W8
                                                                                                              Matches
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GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-93084757; PubMed=1452660;
Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyselaracterization and comparison of Australian human spotted;
Group rickettsiae.";
J. Clin. Microbiol. 30:2896-2902(1992).
EMBL, M99391, AAA73386.1;
SRQÜENCE 154 AA; 15849 MW; F5C35855EDB439D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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Last sequence update)
Last annotation update)
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35.3%; Pred. No. 2.7e-14;
iive 31; Mismatches 54
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1-NOV-1996 (TIEMBLrel. 01, Last sequence
01-CT-2002 (TIEMBLrel. 22, Last annocating (Clone PRB FISF 1), S' end CDS (Fragment)
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Length 131;

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80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                                                                                                                              62 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
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                                                                                                                                                                              25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
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01-OCT-2002 (TERMBLrel. 16, Last sequence update)
17 kDa protein (Fragment).
Rickettsia sp. California 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese; Rickettsiaese
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
                                ch 29.0%; Score 241.5; DB 2; Length 1 1 Similarity 39.1%; Pred. No. 3.7e-14; 50; Conservative 24; Mismatches 43; Indels
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Nilsson K., Pahlson C.,
"Novel peptide diagnostic reagent and kit for detection
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EMBL; AF181036; AAGG9427.1;
NON_TER 151 151
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein (Fragment).
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Pred. No. 7.3e-14;
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35.9%; Pred. No. /...
... 28; Mismatches
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STRAIN=California 2;
Raoult D.;
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                                Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus from Italy.";
Bmerg. Infect. Dis. 8:983-986(2002).
BMBL; AJ427883; CAD20879.1; -.
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"First detection of spotted fever group rickettsiae in Ixodes ricinus
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Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
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MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=184232;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184231;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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23, Last annotation update)
124 GQD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Emerg. Infect. Dis. 8:983-986(2002)
EMBL; AJ427882; CAD20878.1; -.
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131 AA;
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tes 50; Conserv
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80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simser J.A., Palmer A.T., Munderloh U.G., Kurtti T.J.;
"Isolation of a spotted fever group rickettsia, Rickettsia peacockii, in a Rocky Mountain wood tick, Dermacentor andersoni, cell line."; Appl. Environ. Microbiol. 67:546-552(2001).

EMBL; AF26051; AAF69012.1; -.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=47589;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
11-OCT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa surface antigen (Fragment).
Rickettsia peacockii.
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   131 AA
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EMBL; AJ427881; CAD20877.1; -.
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MEDLINE=22182650; PubMed=12194779;
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MEDLINE=21091941; PubMed=11157215;
   PRELIMINARY;
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                                                                                                                                                                                                           Rickettsia helvetica.
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=35789;
                                                          01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                      Query Match 28.4%; Score 236.5; DB 2; Length 131; Best Local Similarity 38.3%; Pred. No. 1e-13; Matches 49; Conservative 24; Mismatches 44; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia sp.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 28.4%; Score 236.5; DB 2; Length 131; Local Similarity 38.3%; Pred. No. 1e-13; nes 49; Conservative 24; Mismatches 44; Indels 11
"A new SFG rickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                           STRAIN=California 2;
Roux V., Raoult D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                                                                                                   131
13374 MW; 23C8819B29FFF860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 AA; 13344 MW; AIDCF71050DF52DF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA
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J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1;
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RESULT 13 Q52637

14 RESULT Q8KLU2

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Gaps

11;

DB 2; Length 131;

Scoring table:

Searched:

Database :

Perfect score:

Sequence:

OM protein

Run on:

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ALIGNMENTS
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1068.647 Million cell updates/sec
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                                                                                                                                        November 5, 2003, 20:12:57; Search time 137.938 Seconds
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| cgn2 6/ptodata71/paa/USO6 COMB.pep:*
2: /cgn2 6/ptodata71/paa/USO6 COMB.pep:*
3: /cgn2 6/ptodata71/paa/USO80 COMB.pep:*
5: /cgn2 6/ptodata71/paa/USO81 COMB.pep:*
6: /cgn2 6/ptodata71/paa/USO81 COMB.pep:*
7: /cgn2 6/ptodata71/paa/USO81 COMB.pep:*
8: /cgn2 6/ptodata71/paa/USO82 COMB.pep:*
9: /cgn2 6/ptodata71/paa/USO85 COMB.pep:*
11: /cgn2 6/ptodata71/paa/USO85 COMB.pep:*
12: /cgn2 6/ptodata71/paa/USO85 COMB.pep:*
13: /cgn2 6/ptodata71/paa/USO89 COMB.pep:*
14: /cgn2 6/ptodata71/paa/USO89 COMB.pep:*
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16: /cgn2 6/ptodata71/paa/USO89 COMB.pep:*
17: /cgn2 6/ptodata71/paa/USO89 COMB.pep:*
18: /cgn2 6/ptodata71/paa/USO89 COMB.pep:*
19: /cgn2 6/ptodata71/paa/USO99 COMB.pep:*
10: /cgn2 6/ptodata71/paa/USO99 COMB.pep:*
10: /cgn2 6/ptodata71/paa/USO94 COMB.pep:*
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12: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
13: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
14: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
15: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
16: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
17: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
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19: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
10: /cgn2 6/ptodata71/paa/USO98 COMB.pep:*
  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Fora, 974 Page これない Seg. 105 2, Ford, V.

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Sequence 22817, A Sequence 19701, A Sequence 19701, A Sequence 4769, Ap Sequence 4769, Ap Sequence 85693, Ap Sequence 16, Appl
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3827, Ap
3363, Ap
10773, A
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Sequence 6,
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Sequence 3
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8 US-10-261-446-2

0 US-09-677-374-4

0 US-09-677-374-6

0 US-09-677-374-6

0 US-09-677-374-6

8 US-10-261-446-6

PCT-USOZ-12532-169

7 US-10-127-032-169

9 US-10-128-12817701

9 US-10-128-12817701

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10 US-10-128-12754

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10 US-10-128-12754

10 US-10-11-128-12754

10 US-10-
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Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Ruzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: KAY, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDC01/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-16
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
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PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18

Score

Result 80.

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APPLICANT: Kuzyk, wichael A.
APPLICANT: Kuzyk, wichael A.
APPLICANT: Kuzyk, wichael A.
APPLICANT: Kuzyk, william W.
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTE FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILLE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SEQ ID NOS: 20
SEQ ID NOS: 20
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SEQ ID NOS: 20
APPLICANT: Kay, William

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: NACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
PRIOR PLILING DATE: 2000-09-18
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PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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Pred. No. 7.8e-81;
1; Mismatches 1;
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Pred. No. 7.8e-81;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.5%;
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Best Local Similarity 98.8%;
Matches 158; Conservative
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Matches 158; Conservative
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APPLICANT: Burian, Jan
APPLICANT: TAY, WILLIAM W.
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT PILLING DATE: 2002-09-30
PRIOR FILLING DATE: 2000-09-15
PRIOR FILLING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 3.8e-83;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                         Query Match
100.0%; Score 836; DB 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-83;
Matches 162; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
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GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
                    SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
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Pred. No. 1.5e-80;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 182
                          PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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; APPLICANT: Whiteley, Marvin
                                                                                                                                                                                                                                             LENGTH: 256
TYPE: PRT
ORGANISM: Piscirickettsia salmonis
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PCT-US02-12532-169
2002-09-30
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 158; Conservative
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LOCATION: (-95)..(-1)
CURRENT FILING DATE:
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Best Local Similarity
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US-10-127-032-169
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Sequence 6, Application US/09677374

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Wichael
APPLICANT: Thornton, Julian
APPLICANT: Trongly VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374

CURRENT FILING DATE: 2000-09-15
PRIOR PLILNG DATE: 1999-09-17
PRIOR APPLICATION NUMBER: NO 2004637
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
AITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
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                                    GGLIGSKIGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                  62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
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                                                                                                                                                             123 ROOYCREFQOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                  122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 ROOYCREFOOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10261446
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-677-374-6
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APPLICANT: NOLLING, JORK
APPLICANT: NOLLING, JORK
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERROR: PATHO3-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2093-02-13
PRIOR PILING DATE: 1999-02-13
     INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 MRKSALIVASFTAMALALGGCQSSLTGDTYSREBARTVQTVRMGTIQALRPVKIEGTKTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 15.4%; Score 128.5; DB 30; Similarity 34.8%; Pred. No. 4e-05; 32; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%; Score 116; DB 29; 25.0%; Pred. No. 0.00078; tive 21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 -KLNOSLEKV------KAGQVTRWRNP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE-
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AND TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 22817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19701, Application US/10366683
GENERAL INFORMATION:
APPLICANT: Rubenfield, Marc J.
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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132 STRAYVQQVDQGQIFR 147
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Best Local Similarity 25.09
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserv
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US-10-366-683-19701
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APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION NUMBER: US/10/366,683
CURRENT APPLICATION NUMBER: US/252,991
PRIOR PILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22817
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        APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
TITLE OF INVENTION: BIOFILM FORMATION
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-024
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.4%; Score 128.5; DB 29; Length 192; Best Local Similarity 34.8%; Pred. No. 4e-05; Matches 32; Conservative 13; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 27; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 128.5; DB 27; Best Local Similarity 34.8%; Pred. No. 3.7e-05; Matches 32; Conservative 13; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 STVHDSSEKVVGYDVKYMLDGKAGQIRMERDP 161
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; Sequence 22817, Application US/10419128
; GREAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22817, Application US/10366683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa US-10-366-683-22817
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-366-683-22817
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Sequence 4769, Application US/10603114
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT PAPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB:
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NOWBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 85693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GAVLGGFLGNTVGGGTGRSLATAAGAVAGGMAGQGVQGAMNRTDGVQLEVRKDDGTTILV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AVAIAAVTLIGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 31; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 113.5; DB 22; 24.7%; Pred. No. 0.0013; ive 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SLIIISVFLVGCAQN-----FSRQE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 114.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 85693, Application US/09791537 GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia enterocolitica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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148 QGQRVAVIGNGNNLTVSP 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.4%;
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 25.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GCLQGSSL-----
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SEQ ID NO 4769
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Matches 37; Conserv
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US-09-791-537-85693
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT PAPLICATION NUMBER: US/09/543,681A
CURRENT PAPLICATION NUMBER: US/09/543,681A
PRIOR PAPLICATION NUMBER: US/09-04-05
PRIOR APPLICATION NUMBER: US/09-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
APPLICANT: MAKE J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AFRICALIS

CURRENT APPLICATION NUMBER: US/10/419,128

CURRENT APPLICATION NUMBER: US/09/252,991

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 MRKSALIVASFTAMALALGGCQSSLTGDTYSREBARTVQTVRMGTIQALRPVKIEGTKTP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL----- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 LFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK-----VKAGQVTRWR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 13.9%; Score 116; DB 30; Length 165; 1 Similarity 25.0%; Pred. No. 0.00078; 34; Conservative 21; Mismatches 41; Indels 4
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; Pred. No. 0.0011;
19; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE---
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAYVQQVDQGQIFR 147
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25.4%;
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Best Local Similarity 25.4
Matches 35; Conservative
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Best Local Similarity
Matches 34; Conserv
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Search completed: November 5, 2003, 20:25:12 Job time : 138.938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2003, 20:13:32; Search time 9.23316 Seconds (without alignments) 824.821 Million cell updates/sec Run on:

US-09-677-374-2 836 Title: Perfect score:

1 MNRGCLQGSSLIIISVFLVG......IYGTACRQPDGRWQVISTEK 162

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

248976 seqs, 47010500 residues Searched:

248976 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending Patents AA New:*

(cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
(cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
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(cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:* 6:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	, Appl:	Appl.	4, Appli	5, Ap	6, A	434,		5133,	605,	49440	7766,	22745	22744	3444,	,699	50, A	6542,	2863,	8, Appl	1229,	403,	I, Ap	8, A	00,	96, A	2773,
Description	Sequence 6	Sequence		_	Sequence 1					-	Sequence						Sequence 1		_	Sequence 1			Sequence	Sequence 1		
QI	US-10-241-602B-6	US-10-261-445B-2	US-10-261-445B-4	US-10-261-445B-6	US-10-261-445B-16	US-09-581-286A-434	US-09-581-286A-309	US-09-897-516A-5133	US-10-389-647-605	US-10-425-114A-49440	US-09-897-516A-7766	US-10-679-063-22745	US-10-679-063-22744	PCT-US03-26780-3444	US-09-674-546A-1669	US-10-435-696-50	US-10-679-063-16542	PCT-US03-28227-2863	PCT/US02/39429-8	US-10-296-115-1229	PCT-US03-28227-5403	PCT-US03-31442-3	PCT-US02-38594-98	PCT-US02-38594-100	PCT-US02-38594-96	US-60-487-610-2773
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Length	162	162	161	256	20	223	230	106	66	734	403	515	517	1755	2599	593	1261	293	423	800	820	871	390	390	404	404
Query	100.0	100.0	97.5	97.5	13.4	12.6	12.6	11.7	10.0	7.6	9.6	9.6	9.6	9.6	9.6	9.4	9.4	9.1	9.1	8.9	8.9			8.8	8.8	8.8
Score	836	836	815	815	112	105.5	105.5	97.5	83.5	-	80	80	80	80	80	79	79	76	92	74	74	74	73.5	73.5	73.5	73.5
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Sequence 4, Appli Sequence 70833, A		71, 7, A	4 ru		1796	Sequence 332, App Sequence 3, Appli	Sequence 6, Appli	Sequence 4405, Ap	Sequence 14, Appl	Sequence 22287, A	Sequence 2783, Ap	Sequence 1525, Ap
US-09-743-818A-4 US-10-425-114A-70833	FCI-0503-106558-5 PCT-US03-26780-2711 US-10-689-006-24	US-09-743-818A-71 US-09-743-818A-7	PCT-US02-24483-40 US-09-743-818A-5	PCT-US02-24483-38	US-60-487-610-1796	US-10-4/2-928-932 PCT-US03-32968-3	PCT-US03-32968-6	US-09-897-516A-4405	US-08-592-070D-14	US-10-679-063-22287	US-60-487-610-2783	US-60-487-610-1525
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73.5	73	72.5	72.5	72.5	72.5	7.2	72	72	72	72	72	72
23	30	3 3 3	3.34 5.54	36	37	9 6	40	41	42	43	44	45

### ALIGNMENTS

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61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
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                                                                                              APPLICANT: STUMENT, MALIALIE
APPLICANT: BOUNDERS, Simon
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Greeve
APPLICANT: Walenzuela, Pablo
APPLICANT: Burzio, Luis
TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
FILE REFERENCE: H-32319A
CURRENT APPLICATION NUMBER: US/10/241,602B
CURRENT FILING DATE: 2002-09-11
PRIOR PLING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: GB0005838.8
PRIOR PLING DATE: 2000-07-01
PRIOR APPLICATION NUMBER: GB0016080.4
PRIOR PLING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
PRIOR PLING DATE: 2000-07-01
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100.0%; Pred. No. 6.4e-65;
iive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                        Sequence 6, Application US/10241602B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 162, Conservative
                                                                          APPLICANT: Simard, Nathalie
US-10-241-602B-6
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APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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APPLICANT: MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MISTA, MIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GGLIGSKIGQSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                            62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
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2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
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                                                                                                                                                                                                                                                                                       122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                          123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 815; DB 6;
Pred. No. 7.1e-63;
1; Mismatches 1.
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-261-445B-6; Sequence 6, Application US/10261445B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
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; LOCATION: (-95)..(-1)
US-10-261-445B-6
                                                                                  63
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                                                                                                                                   ## APPLICANT: Kuzyk, Michael A.

## APPLICANT: Kuzyk, Michael A.

## APPLICANT: Burian, Jan

## APPLICANT: Burian, Jan

## APPLICANT: Burian, Jan

## APPLICANT: Burian, Jan

## APPLICANT: Thornton, Julian C.

## TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST.

## TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY

## TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY

## CURRENT APPLICATION NUMBER: US/10/261,445B

## CURRENT APPLICATION NUMBER: US 09/677,374

## PRIOR PILING DATE: 2000-09-15

## PRIOR PILING DATE: 1999-09-17

## PRIOR PILING DATE: 1999-09-17

## NUMBER OF SEQ ID NOS: 20

## SOFTWARE: Patentin version 3.0
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APPLICANT: Ray, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
ITILE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
ITILE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 836; DB 6;
100.0%; Pred. No. 6.4e-65;
rative 0; Mismatches 0;
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97.5%; Score 815; DB 6;
Best Local Similarity 98.8%; Pred. No. 4.1e-63;
Matches 158; Conservative 1; Mismatches 1
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                              Sequence 2, Application US/10261445B GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 162; Conservative
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US-10-261-445B-4
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LENGTH: 162
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NUMBER OF SEQ ID NOS: 20

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RESULT 8
US-09-897-516A-5133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2000-06-28

FRIOR APPLICATION NUMBER: PCT/AU98/01023

PRIOR FILING DATE: 1998-12-10

PRIOR FILING DATE: 1998-12-10

PRIOR FILING DATE: 1997-12-10

PRIOR FILING DATE: 1997-12-31

PRIOR PELING DATE: 1997-12-31

PRIOR PELING DATE: 1998-03-10

PRIOR PELING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-10

PRIOR PELING DATE: 1998-03-10

PRIOR PELING DATE: 1998-03-10

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-05-05

PRIOR PELING DATE: 1998-05-05

PRIOR PELING DATE: 1998-05-05

PRIOR PELING DATE: 1998-05-05

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PRIOR PELING DATE: 1998-05-05

PRIOR PELING DATE: 1998-07-05

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                                                                                                                                                                                                                                                       Query Match
13.4%; Score 112; DB 6; I
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 20; Conservative 0; Mismatches 0;
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36.1%; Pred. No. 0.06;
tive 12; Mismatches
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GENERAL INFORMATION:
APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: ROTHEL, LINDA J.
APPLICANT: ROTHEL, LINDA J.
APPLICANT: MARGETTS, MAL B.
APPLICANT: WOCKING, DIANNA M.
APPLICANT: WEBB, ELIZABETH A.
                                                                                                            ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-445B-16
                                                                                                                                                                                                                                                                                                                                                                                                      110 PVRTYQRYNKQERRQQYCRE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 20
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Best Local Similarity 36.1%
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66 ALIGKKMDKOKK 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-581-286A-434
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APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: MAL B.
APPLICANT: HCKING, DIANNA M.
TILLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
TILLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/581,286A
CURRENT RILING DATE: 1998-12-10
PRIOR PELLING DATE: 1998-12-10
PRIOR PELLING DATE: 1997-12-10
PRIOR PELLING DATE: 1997-12-31
PRIOR PELLING DATE: 1998-01-30
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PRIOR PELLING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: AU PP 2264
PRIOR APPLICATION NUMBER: AU PP 211
PRIOR APPLICATION NUMBER: AU PP 3128
PRIOR APPLICATION NUMBER: AU PP 3138
PRIOR PELLING DATE: 1998-05-05
PRIOR PELLING DATE: 1998-05-05
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OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - See File Wrapper or PALM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 721
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
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Sequence 309, Application US/09581286A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Porphyromonas gingivalis
US-09-581-286A-309
                                                                   APPLICANT: ROSS, BRUCE C.
PRELICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin version 3.2
SEQ ID NO 309
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Best Local Similarity 36.1%
Local Similarity 36.1%
Local Similarity 36.1%
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137 VIADGNGVTEGQEDHCLKNETVNNVVA-----NADEGNSGAVECFQTYKRKHAKSSS 189
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Stater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Kenchabdus sp. Genome Sequences And Uses Thereof FILE, REFERENCES: 38-21(51847) B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                                                                Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 403;
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                                                                                                                                                                                                                                                                                                                                DB 6;
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Best Local Similarity 34.2%; Pred. No. 19;
Matches 26; Conservative 11; Mismatches 3:
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 700991377_FLI.pep
US-10-425-114A-49440
                                                                                                                                                                                                                                                                                                                              Query Match 9.7%; Score 81.5; D
Best Local Similarity 25.5%; Pred. No. 29;
Matches 35; Conservative 24; Mismatches
CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 SEQ ID NOS: 73128 LENCYH: 734 TYDPP.
                                                                                                                                                                                                                                                                                                                                                                                                                              26 SRQEVGAATGAVVGGVA--GQLFGKGSGRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7766, Application US/09897516A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-679-063-22745; Sequence 22745, Application US/10679063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 QY-CREFQQKAMIAGQK 140
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                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With IIILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω,
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                                                                                                                                                                                                                                                                                                                                                                               9; Gaps
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                                                                                                                                                                                                                                                                                                                         Score 97.5; DB 5; Length 106;
Pred. No. 0.12;
8; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.0%; Score 83.5; DB 6; Length 99; Best Local Similarity 32.9%; Pred. No. 1.8; Matches 23; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCOMMENTATION:

APPLICANT: GREENERG, E. Peter
APPLICANT: GCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
CURRENT APPLICATION NUMBER: US/10/389, 647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 605
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                         28 QEVGAATGAVVGGVAGQLFGKGS--GRVAMAIGGAVLGGLIGSKI--
                                                             CURRENT APPLICATION NUMBER: US/09/897,516A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 60/215,161 PRIOR FILING DATE: 2000-06-30 NUMBER OF SEQ ID NOS: 8415 LENGTH: 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KTKIYTSTQVGRTCQFT 80
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.4%;
Matches 28; Conservative
                                         FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                      ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 -GAVLGGLIG 67
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61 MGAIAGGTVG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-114A-49440
                                                                                                                                                                                                                                                                            US-09-897-516A-5133
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; ORGANISM: Homo sapiens
PCT-US03-26780-3444
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APPLICANT'S FIVERPRINE THERAPEUTICS, INC.
APPLICANT'S FIVERPRINE THERAPEUTICS, INC.
APPLICANT'S FIVERPRINE THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYEPPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TILE OF INVENTION: THEIR USE
FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: PO.203-08-29
FRIOR APPLICATION NUMBER: 60/406,616
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
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FRIOR APPLICATION NUMBER: 60/406,655
FRIOR APPLICATION NUMBER: 60/406,642
                                                                                                                                                                                                                                                                                                                                                                                                                     45 VAGNLHEGGMKKVVAARRPVLGELGNKVLRNASQDLLGKGVEKGAALKNANPTLKNIKPR 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
RIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22744
                                                                                                                                                                                                                                                                                      9.6%; Score 80; DB 6; Length 515;
28.1%; Pred. No. 25;
tive 15; Mismatches 41; Indels
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FILE REFERENCE: 38-15 (52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
LENGTH: 515
                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-679-063-22745
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12-10-679-063-22744
1 Sequence 22744, Application US/10679063
5 GENERAL INFORMATION:
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US-10-679-063-22744
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Best Local Similarity 28.1*
Matches '25, Conservative
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Matches 25; Conservative
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APPLICANT: Chiron Corporation
TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
FILE REFERENCE: CHIR-0334
                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 3700
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19.3%; Pred. No. 1.7e+02;
tive 32; Mismatches 45; Indels
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 5, 2003, 20:25:58 Job time: 10.2332 secs
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PRIOR APPLICATION NUMBER: 60/406,640
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,576
PRIOR APPLICATION NUMBER: 60/406,646
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
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PRIOR APPLICATION NUMBER: 60/406,653
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SEQ ID NO 3444
LENGTH: 1755
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Matches 40, Conservative
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Best Local Similarity 43.99
Matches 18, Conservative
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                      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Sequence 4, Appli

161 20 US-09-677-374-4

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Description

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is Sequence 4, Application US/09677374
is Sequence 4, Application US/09677374
is General Information:
APPLICANT: Burian, Jan
APPLICANT: Kazyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Kay, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDC01/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR PELICATION NUMBER: US 60/154,437
PRIOR PELICATION NUMBER: US 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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NUMBER OF SEQ ID NOS: 20
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Sequence 2, Appli
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TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCOJ/60485/US
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-16
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 832; DB 20;
Best Local Similarity 100.0%; Pred. No. 8.3e-83;
Matches 161; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
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ORGANISM: Piscirickettsia salmonis
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ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10261446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 20
SOFWWARE: PatentIn version 3.0
SEQ ID NO ELENGTH: 256
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; LOCATION: (-95)..(-1)
US-09-677-374-6
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LOCATION: (-95)..(-1)
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APPLICANT: Ray, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETFSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/061,446
CURRENT FILING DATE: 2002-09-30
PRIOR FILING DATE: 2000-09-15
PRIOR PLICATION NUMBER: US 60/154,437
PRIOR PLING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                    Query Match 100.0%; Score 832; DB 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 832; DB 28;
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 161; Conservative 0; Mismatches 0;
                                                                                      ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-09-677-374-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Piscirickettsia salmonis
US-10-261-446-4
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 161
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APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
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APPLICANT: Burian, Jan
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RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
FILE REPERENCE: UIZ-O7GCPC.
CURRENT APPLICATION NUMBER: PCT/US02/12532
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR PILING DATE: 2001-04-29
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
98.0%; Score 815; DB 28;
Best Local Similarity 98.8%; Pred. No. 3.4e-81;
Matches 158; Conservative 1; Mismatches 1;
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                                  FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR PILING DATE: 1099-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US02-12532-169; Sequence 169, Application PC/TUS0212532; GENERAL INFORMATION:
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; APPLICANT: Whiteley, Marvin
                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
PCT-US02-12532-169
              TITLE OF INVENTION:
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US-10-127-032-169
                                                                                                                                                                                                                                                                                                                 LENGIH: 162
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                                                                                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Unlian
APPLICANT: Thornton, Unlian
APPLICANT: Thornton, Unlian
ITILE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
ITILE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
ITILE OF INVENTION: NUMBER: US/09/677,374
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
PRIOR PLILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jun
APPLICANT: Ray, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
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                                                                                                                             96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                      156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
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                                                                                                                                                                                                       LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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                                                                                              1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
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                                          0; Gaps
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                216 RROQYCREFQOKAMIAGGKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                   121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ROOYCREFOOKAMIAGOKQEIYGTACPOPDGRWOVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.3e-83; 
; Mismatches 0;
100.0%; Pred. wc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-677-374-2
; Sequence 2, Application US/09677374
; GENERAL INFORMATION:
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Best Local Similarity 98.8*
Matches 158; Conservative
                                       Matches 161; Conservative
           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
15.3%; Score 127.5; DB 30;
Best Local Similarity 34.8%; Pred. No. 4.8e-05;
Matches 32; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 -KLNQSLEKV-----KAGQVTRWRNP 99
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                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa US-10-419-128-22817
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US-09-543-681A-4769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Conservative
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Best Local Similarity
Matches 35; Conserv
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US-09-543-681A-4769
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US-10-603-114-4769
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APPLICANT: NOTHING, JORK
APPLICANT: NOTHING, JORK
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH03-04
CURRENT APPLICATION NUMBER: US/10/366,683
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR APPLICATION NUMBER: 09/252,991
NUMBER OF SEQ ID NOS: 33142
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           APPLICANT: LOTY, Stephen
APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
TITLE OF INVENTION: BIOFILM FORMATION
CURRENT APPLICATION WHABER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-40
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 182
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GENERAL INFORMATION:
APPLICANT: Rubenfield, Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22817, Application US/10419128 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-169
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Best Local Similarity 34.8%
Matches 32; Conservative
Bangera, M. Gita
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US-10-419-128-22817
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LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
APPLICANT:
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Sequence 4769, Application US/09543681A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIJ
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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GENERAL INFORMATION
PAPILOANT: GARY BREION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURENT APPLICATION NUMBER: US/10/419,128 CURENT APPLICATION NUMBER: US/10/419,128 CURENT APPLICATION NUMBER: US/09/252,991 PRIOR APPLICATION NUMBER: US/09/252,991 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 22817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 139
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APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERBUCE: 1DCO-9-15
CURRENT FILING DATE: 2000-09-15
PRIOR PPLICATION NUMBER: US 60/154,437
PRIOR PPLICATION NUMBER: US 2000-09-15
PRIOR APPLICATION NUMBER: E 2000/0752
PRIOR APPLICATION NUMBER: G 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PPLING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: G 2544-2000
PRIOR APPLICATION NUMBER: G 2544-2000
PRIOR APPLICATION NUMBER: C 2544-2000
PRIOR PLING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 20
SOCTWARE: Patentin version 3.0
SOCTWARE: Patentin version 3.0
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; Sequence 16, Application US/10261446
; GENERAL INFORMATION:
; APPLICANT: Kuzyk, Michael A.
; APPLICANT: Burian, Jan
; APPLICANT: Ray, William W.
; APPLICANT: Thornton, Julian C.
; TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
; TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
; FILE REFERENCE: 4616-64094
; CURRENT APPLICATION NUMBER: US/10/261,446
; CURRENT APPLICATION NUMBER: US 09/677,374
; PRIOR PELING DATE: 2000-09-15
; PRIOR FILING DATE: 1099-09-17
; NUMBER OF SEQ ID NOS: 20
; SOFFWARE: Patentin version 3.0
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100.0%; Pred. No. 0.00011;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Piscirickettsia salmonis
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Best Local Similarity 100.0
Matches 20; Conservative
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 85693
LENGTH: 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK-----VKAGQVTR 95
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Best Local Similarity 24.7%; Pred. No. 0.0016;
Matches 37; Conservative 19; Mismatches 43; Indels 51;
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                       DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 114.5; DB 3 25.0%; Pred. No. 0.0011;-:ive 20; Mismatches 54
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                                                  FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
FRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-677-374-16; Sequence 16, Application US/09677374; GENERAL INFORMATION:
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; ORGANISM: Yersinia enterocolitica
US-09-791-537-85693
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.0 Matches 35, Conservative
                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 166
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;; Search time 9.17617 Seconds (without alignments) 824.821 Million cell updates/sec US-09-677-374-4 832 1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161 20:13:32 Title: Perfect :

score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

248976 seqs, 47010500 residues

Searched:

248976

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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No.	Score	Match	Match Length	BB	σι	Description
-	832	100.0	161	ø	US-10-261-445B-4	Sequence 4, Appli
~	832	100.0	256	ø	US-10-261-445B-6	9
e	815	98.0	162	9	US-10-241-602B-6	ý
4	815	98.0	162	9	US-10-261-445B-2	Sequence 2, Appli
2	112	13.5	20	9	US-10-261-445B-16	16,
9	102.5	12.3	223	S	US-09-581-286A-434	434
7	102.5	12.3	230	'n	US-09-581-286A-309	309,
80	94.5	.11.4	106	Ŋ	US-09-897-516A-5133	5133,
6	86.5	10.4	66	9	US-10-389-647-605	Sequence 605, App
10	83	10.0	423	٦	PCT/US02/39429-8	8, 4
11	82.5	9.6	734	9	US-10-425-114A-49440	
12	79.5	9.6	1117	-	PCT-US03-21510-114	
13	79	9.5	593	9	US-10-435-696-50	
14	79	9.5	1261	9	US-10-679-063-16542	
15	78.5	9.4	261	9	US-10-689-006-24	• •
16	78	9.4	403	ß	US-09-897-516A-7766	
17	78	9.4	438	Н	PCT-US02-39429-88	
18	78	9.4	515	9	US-10-679-063-22745	
19	78	9.4	517	9	US-10-679-063-22744	Sequence 22744, A
20	77	9.3	1755	Н	PCT-US03-26780-3444	Sequence 3444, Ap
21	77	9.3	2599	'n	US-09-674-546A-1669	Sequence 1669, Ap
22	73	8.8	254	~	PCT-US03-10856A-5	5, App
23	73	8.8	293	Н	PCT-US03-28227-2863	286
24	73	8.8	800	9	US-10-296-115-1229	Sequence 1229, Ap
25	73	8.8	820	-	PCT-US03-28227-5403	Sequence 5403, Ap
26	73	8.8	871	-	PCT-US03-31442-3	

Sequence 6, Application US/10261445B; GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
SAPLICANT: Burian, Jan
APPLICANT: Kay, William W.

RESULT 2 US-10-261-445B-6

Sequence 2711, Ap	Sequence 19, Appl	Sequence 7732, Ap	Sequence 64061, A	Sequence 52050, A	Sequence 77, Appl	Sequence 418, App	Sequence 59401, A	Sequence 3, Appli	Sequence 128, App	Sequence 4797, Ap	Sequence 4, Appli	Sequence 38, Appl	Sequence 2779, Ap	Sequence 4796, Ap	Sequence 932, App	Sequence 43688, A	Sequence 72589, A	Sequence 20, Appl
PCT-US03-26780-2711	US-10-435-614-19	US-10-679-063-7732	US-10-425-114A-64061	US-10-425-114A-52050	US-10-418-861B-77	US-60-499-964-418	US-10-425-114A-59401	US-09-830-321A-3	US-09-976-858-128	PCT-US03-28227-4797	US-09-743-818A-4	PCT-US03-18234-38	US-60-487-610-2779	PCT-US03-28227-4796	US-10-472-928-932	US-10-425-114A-43688	US-10-425-114A-72589	US-10-435-614-20
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2322	260	348	429	596	1064	181	315	456	456	069	733	798	798	838	83	224	230	260
8.8	8.7	8.7	8.7	8.7	8.7	9.8	8.6	8.6	8.6	8.6	8.6	8.6	9.8	8.6	8.5	8.5	8.5	8.5
73	72.5	72.5	72	72	72	71.5	71.5	71.5	71.5	71.5	71.5	71.5	71.5	71.5	71	71	71	71
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: BUTIAN, MINISTER APPLICANT: BUTIAN, MINISTER APPLICANT: BUTIAN, Jan APPLICANT: BUTIAN, JAIN APPLICANT: Thornton, Julian C.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VARIED: 1999-09-17
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 832; DB 6;
100.0%; Pred. No. 3.2e-66;
ive 0; Mismatches 0;
                                       Sequence 4, Application US/10261445B; GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 161, Conservative
RESULT 1
US-10-261-445B-4
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Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
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US-10-261-445B-16
                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-10-261-445B-2
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## APPLICANT: Thornton, Julian C.

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY

FILE REPERENCE: 4616-64095

CURRENT PELICATION NUMBER: US/10/261,445B

CURRENT PELING DATE: 2002-09-30

FRIOR APPLICATION NUMBER: US 60/57,374

PRIOR APPLICATION NUMBER: US 60/154,437

PRIOR PILING DATE: 1999-09-17

WINDER OF SEQ ID NOS: 20

SOFTWARE: PATENTING PATE: 1999-09-17

SOFTWARE: PATENTING DATE: 1999-09-17

SOFTWARE: PATENTING DATE: 1999-09-17

MUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 6

SEQ ID NO 6

TYPE: PRT

ORGANIGN: Piscirickettsia salmonis
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APPLICANT: Brouwers, Huub
APPLICANT: Brouwers, Huub
APPLICANT: Glores, Simon
APPLICANT: Gliffiths, Steve
APPLICANT: Gliffiths, Steve
APPLICANT: Gliffiths, Steve
APPLICANT: Burzio, Luis
APPLICANT: Burzio, Luis
CURRENT BURZON: Luis
CURRENT PILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: C2002-09-11
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-07-01
PRIOR APPLICATION NUMBER: GB0016080.4
PRIOR PILING DATE: 2000-07-01
PRIOR PILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
SRIOR APPLICATION NUMBER: GB0016082.0
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
SEQ ID NOS: 34
SOFTWARER: PASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 832; DB 6; Length 256; 100.0%; Pred. No. 5.5e-66; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10241602B
GENERAL INFORMATION:
APPLICANT: Simard, Nathalie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: SIGNAL
; LOCATION: (-95)..(-1)
US-10-261-445B-6
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APPLICANT: Burian, Jan
APPLICANT: Eurian, Jan
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFREENCE: 4616-641095
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Burian, Jan
APPLICANT: RAY, William W.
APPLICANT: RAY, William W.
APPLICANT: KAY, WILLIAM W.
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: WICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US/0/261,445B
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/17,374
PRIOR FILING DATE: 1299-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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                                                                                         GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                           63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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Gaps
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Pred. No. 1e-64;
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                                                                                                                                                                                                                                                                                   123 ROCYCREFOCKAMIAGCKOEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                     122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10261445B GENERAL INFORMATION:
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Query Match
Best Local Similarity 34.7%
Matches 25, Conservative
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APPLICANT: BARR, IAN G.
APPLICANT: BARR, IAN G.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: MARGETTS, MAL B.
APPLICANT: MARGETTS, MAL B.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: WEBB, ELIZABETT A.
ITITE ROFERENCE: 4137.
ITITE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
CURRENT FILING DATE: 1990-12-10
PRIOR PRIOR APPLICATION NUMBER: AU PP 0839
PRIOR FILING DATE: 1997-12-31
PRIOR PILING DATE: 1997-12-31
PRIOR PLING DATE: 1999-01-30
PRIOR PLING DATE: 1999-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-05-05
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NUMBER OF SEQ ID NOS: 721
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                               Ouery Match
13.5%; Score 112; DB 6; I
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 20; Conservative 0; Mismatches 0;
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ORGANISM: Porphyromonas gingivalis
                                                                                                                              ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-445B-16
                                                                                                                                                                                                                                                                                                                                                                                                    109 PVRTYQRYNKQERRQQYCRE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PVRTYQRYNKQERRQQYCRE 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 20
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66 ALIGKKMDKQKK 77
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LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 CVSGGTL---SGMIVGAVD-----GAATGMAIGGKWGGAGGFGFGALSQLVGLIVPTA 60
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                           Score 94.5; DB 5; Length 106;
Pred. No. 0.16;
9; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.4%; Score 86.5; DB 6; Length 99; Best Local Similarity 34.3%; Pred. No. 0.74; Matches 24; Conservative 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-389-647-605
; Sequence 605, Application US/10389647
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: GREENERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candi
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: UIS-038CP
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR PILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                      27 QEVGAATGAVVGGVAGQLFGKGS--GRVSMAIGGAVLGGLIGSKI----
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 5133
LENGTH: 106
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 605
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APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Jin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Rano, John M.
APPLICANT: Beno, John M.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                   78 KIKLNOSLEKVKAGOVT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                     KTKIYTSTQVGRTCQFT 80
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.1%;
Matches 27; Conservative
                                                                                                                                                              TYPE: PRT ORGANISM: Xenorhabdus sp.
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61 MGAIAGGTVG 70
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FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- genc
PCT/US02/39429-8
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
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APPLICANT: Saboriated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GSSPKPWIYATSNLASGVPARFSGSGSGTSYSL----TISRVEAEDAATYYCQQWISNPP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83; DB 1; Length 423;
Pred. No. 8.7;
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERRNCE: 690022.54701PC CURRENT APPLICATION NUMBER: PCT/US02/39429 CURRENT APPLICATION NUMBER: PCT/US02/39429 SOFTWAREN FILING DATE: 2002-12-06 SEQ ID NOS: 92 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 TFGAGTKLELKSSGSGADPSKDSKAQVSAAE 278
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US-10-425-114A-49440
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9.9%; Score 82.5; Di
Best Local Similarity 25.5%; Pred. No. 19; Matches 35; Conservative 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%;
21.7%;
                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.7%;
Matches 33; Conservative
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US-10-425-114A-49440
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88 SYGSSSFGGSYGGSFGGGSFGGGSFGGGFGGGFGGGFGGFGGFGGF--GGLLSGN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 ------SQEDHIRIRTKWHPVLAGELDAWR------LSLNPAQ--QAYLQEKKRISY 301
-GRVSMAIGGAVLGGLIGSKIGQSMDQQ 76
                                                                                                77 DKI-----KINQSLEKVKA------GOVTRWRNPDTGNSYSVEPVRTYQRYNK 118
                                                                                                                                               146 EKVTMQNLNDRLASYLDKVRALEESNYELBGKIKEWYEKH-GNSHQGEP-RDYSKYYK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Hallahan, Dennis E
APPLICANT: Mernaugh, Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
FILE REPERENCE: 1242/72
CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT APPLICATION NUMBER: US/089/914,605
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
SOSTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GAATGAVVG------GVAGQLFGKGSG-----RVSMAIGG-----AVLGGLI
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                                                                                                                                                                                                                                                                                                               APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFERENCE: 38-15(52054) B
CURRENT APPLICATION NUMBER: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 79; DB 6; Length 1261;
24.8%; Pred. No. 73;
tive 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
US-10-689-006-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4%; Score 78.5; 1 19.3%; Pred. No. 12;
  23 NFSRQEVGAATGAVVGG--VAGQLFGKGS-
                                                                                                                                                                                                                                                   US-10-679-063-16542
; Sequence 16542, Application US/10679063
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10689006 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Magnetococcus sp. MC-1
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Best Local Similarity 19.3%
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.8%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial
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US-10-689-006-24
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LENGTH: 261
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          Sequence 114, Application PC/TUS0321510

GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MP21S AS MODIFIERS OF THE D21 PATHWAY AND METHODS OF USE
TITLE OF INVENTION: MP21S AS MODIFIERS OF THE D21 PATHWAY AND METHODS OF USE
CURRENT APPLICATION NUMBER: PCT/US03/21510
CURRENT FILING DATE: 2003-07-09
PRIOR FILING DATE: 2002-07-10
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-130
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PALCENTIN VENSION 3.2
SEQ ID NO 114

LEASTH: 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 NISTSNIPSAAGVSVGPGVTSGVNVNILSGMGNGTISSSAAVSSVPNAAAGMTGGSVSSQ 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 QOQPTVNTSRFRVVKLDSSSEPFKKGRWTCTEFYEKENAVPATEGVLINKVVETVKQNPI 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 QVTRWRNPDTGNSYSVEPVRTYQRYNK-------QERRQQYCREFQQKAMIAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 NFSRQEVGAATGAVVG-GVAGQ-----LFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQ 76
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GENERAL INFORMATION:
APPLICANT: Wirtz, Ralph
APPLICANT: Wunnes, Marc
APPLICANT: Kallabis, Marc
APPLICANT: Kallabis, Marc
APPLICANT: Kallabis, Marc
APPLICANT: Kallabis, METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAC
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.6%; Score 79.5; DB 1; I Best Local Similarity 21.2%; Pred. No. 57; Matches 41; Conservative 25; Mismatches 60;
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CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP0201312.4
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 314
SOFTWARE: Patentin version 3.1
SEQUINO 50
LENGTH: 593
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560 TLQQMDFGSTGPQ 572
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ORGANISM: Homo sapiens
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US-10-435-696-50
  PCT-US03-21510-114
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US-10-435-696-50
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                                                                                                                 November 5, 2003, 20:12:57; Search time 217:976 Seconds (without alignments) 1068.647 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                  5728757 segs, 909918778 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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JOACHEAL INFORMATION:

Sequence 6, Application US/09677374
GENERAL INFORMATION:

APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: KAY, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDC01/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR PLLING DATE: 2000-09-15
PRIOR PLLING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 65163, A
Sequence 19761, A
Sequence 124659,
Sequence 6661, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6661, Ap
Sequence 17654, A
Sequence 17654, A
Sequence 17613, A
Sequence 74713, A
Sequence 84844, A
Sequence 84844, A
Sequence 106665,
                                                                                                                                 Sequence 10, Appl
Sequence 6, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 22, Appli
Sequence 2, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 8, Appli
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Sequence 9, Appli
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B US-10-261-446-6

US-09-677-374-4

US-10-261-446-4

US-10-261-446-2

B US-10-261-446-2

B US-10-261-446-2

B US-10-261-446-2

B US-00-00708-10

PCT-US00-00708-10

PCT-US00-00708-10

PCT-US00-00708-10

US-09-808-898-22

US-09-808-898-22

US-09-808-888-22

US-08-965-888-2

US-08-965-888-2

US-08-965-988-2

US-08-965-988-2

US-09-91-537-105096

US-09-91-537-105096

US-09-91-537-105092

US-09-91-537-105093

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US-09-791-537-105093

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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 1DCO1/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT PILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: IE 2000/0752
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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APPLICANT: Kay, William W.
APPLICANT: Kay, Juliam W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
                                                                                240
                                                                                                                                                                                                181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT 240
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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Best Local Similarity 100.0%; Pred. No. 2.4e-78;
Matches 161; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                 241 ACPÓPDGRWQVISTEK 256
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US-10-261-446-4
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: TACATOR, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 69/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                Length 256;
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                                                                                                                                                                                                                                                                             DB 20;
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ORGANISM: Piscirickettsia salmonis
                                                                                                             ORGANISM: Piscirickettsia salmonis
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GENERAL INFORMATION:
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  SOFTWARE: PatentIn version 3.0
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; LOCATION: (-95)...
US-10-261-446-6
                                                                                                                                      ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (-95)...
US-09-677-374-6
                               SEQ ID NO 6
LENGTH: 256
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LENGTH: 256
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Sequence 2, Application US/10261446

Sequence 2, Application US/10261446

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: WINGER: US/10/261,446
CURRENT APPLICATION NUMBER: US/20-20-30
CURRENT PILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOUTHARE PATENTING DATE: 1090-09-17
NUMBER OF SEQ ID NOS: 20
SOUTHARE PATENTING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
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63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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GENERAL INFORMATION:
APPLICANT: Levy, Ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
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                                                                  217 ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 256
                                                                                                                              123 ROGYCREFOCKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
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Pred. No. 1.5e-76;
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Best Local Similarity 46.8%; Pred. No. 5.2e-42;
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CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOTWARE: Patentin version 3.0
SEQ ID NO 4
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Best Local Similarity 98.8%;
Matches 158; Conservative
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Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kayzk, Michael
APPLICANT: Thornton, Julian
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE OF INVENTION NUMBER: US/09/677,374

CURRENT APPLICATION NUMBER: US 60/154,437

PRIOR APPLICATION NUMBER: IE 2000/0752

PRIOR PILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: EB 000-09-18

PRIOR PILING DATE: 2000-09-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
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Pred. No. 1.5e-76;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.3%; Score 832; DB 28; Best Local Similarity 100.0%; Pred. No. 2.4e-78; Matches 161; Conservative 0; Mismatches 0;
                        CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US 09/677,374
FRIOR APPLICATION NUMBER: US 60/154,437
FRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Piscirickettsia salmonis
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ORGANISM: Piscirickettsia salmonis
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Best Local Similarity 98.8%;
Matches 158; Conservative 1
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SEQ ID NO 2
LENGTH: 163
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                                                        61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                               121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                       181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                         112 -----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-------KVTGYIGGAK--VL 153
1 MSVEFYNSNKSAQINSITPIIKIINTSDSDLNLNDVKVRYYYTSDGTQQQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Levy, llan
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENY APPLICATION NUMBER: PCT/US00/00708
CURRENY FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 326
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.5%; Score 487; DB 1; Length 326; 46.8%; Pred. No. 1.1e-41; Live 12; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (30)...(208)
OTHER INFORMATION: taken from Clostridium cellulovorans
                                                                             61 LGNSYVDNTSKVTANFVKETASPISTYDTYVE----
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PCT-US00-00708-10
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PCT-US00-00708-6

RESULT

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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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Sequence 6, Application PC/TUS0000708

GENERAL INFORMATION:
APPLICANT: Levy, ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
APPLICANT: Nussinovitch, Amos
APPLICANT: Nussinovitch, Amos
PITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Levy, / ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REPERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT FILING DATE: 2000-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Pred. No. 1.1e-41;
9; Mismatches 14; Indels
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36.5%; Score 487; DB 1;
Best Local Similarity 46.8%; Pred. No. 1.2e-41;
Matches 116; Conservative 12; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; Clostridium cellulovorans PCT-US00-00708-6
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 51.7%;
Matches 106; Conservative
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                             DB 23;
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; Pred. No. 7e-41;
10; Mismatches 33;
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APPLICANT: Yosef, Karmey
APPLICANT: Shpisel, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: METHODS OF DETECTION USING
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/330,394
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LEGLIE
REFERENCE/DOCKET NUMBER: 7809-005
                   PRIOR FILING DATE: 1996-11-25
PRIOR APPLICATION WUMBER: 08/597,274
PRIOR FILING DATE: 1996-02-06
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LA LUDRESS:
SIRET: PENNIE & EDMONDS
SIRET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  APPLICATION NUMBER: 08/757,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-06-330-34-2
Sequence 2, Application US/08330394
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                          36.0%;
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TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                    ; ORGANISM: Gaussia
US-09-808-898-22
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Simi
Matches 107;
                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 8
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Sequence 22, Application US/09808998

GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANTION: RENILIAR RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING T
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128

CURRENT PAPLICATION NUMBER: 60/189,691

PRIOR PILING DATE: 2001-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 1999-03-26
121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 MSVEPYNSNKSAQTNSITPIIKITNISDSDLNLNDVKVRYYYTSDGTGGTFWCDHAGAL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS0000708
Sequence 8, Application PC/TUS0000708
GENERAL INFORMATION:
APPLICANT: Levy, 11an
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE 0P INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%; Score 483; DB 1; Length 426;
51.7%; Pred. No. 4.4e-41;
tive 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
| LOCATION: (1)..(263)
| OTHER INFORMATION: protein A from cloning vector NAME/KEY: misc_feature
| LOCATION: (265)..(426)
| OTHER INFORMATION: CBPA | PCT-US00-00708-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-----
                                              -----FGFASGRATL
                                                                                          181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GRITKSDWSNYTQTNDYSFD 400
                                                                                                                                     ----GRITKSDWSNYTQTNDYSFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: recombinant protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                r-US00-00708-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-808-898-22
                                                                                                                                     118
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SEQ ID NO 2
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                                                                                                                                                                                               1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                                                                                                                                                                                                          6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                          0; Gaps
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                                                                                                            Query Match 35.7%; Score 477; DB 7; Length 162; Best Local Similarity 97.8%; Pred. No. 4.7e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shoseyov, oded
APPLICANT: Shoseyov, oded
APPLICANT: Shpiegl, Etai
APPLICANT: Roiz, Levasa
TITLE OF INVENTION: METHODS FOR USE OF A CELLULOSE
TITLE OF INVENTION: BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,588
FILING DATE:
APPLICATION NUMBER: 08/537,893
FILING DATE:
APPLICATION NUMBER: PCT/US94/04132
FILING DATE:
APPLICATION NUMBER: PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             66 LGNSYVDNTSKVTANFVKETASPISTYDTYVE 97
                                                                                                                                                                                                                                                                                      61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MISROCK, S. LESILE
REFERENCE/DOCKET NUMBER: 7809-017
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-962-588-2; Sequence 2, Application US/08962588; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 162 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.8
Matches 90; Conservative
                                       ; MOLECULE TYPE: protein US-08-330-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036
                    TOPOLOGY:
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APPLICANT: Meriah, Ronald A
APPLICANT: Mehigh, Richard J
APPLICANT: Mehigh, Richard J
APPLICANT: Mehigh, Richard J
APPLICANT: Brockie, Ian
APPLICANT: Brockie, Ian
APPLICANT: Brockie, Ian
APPLICANT: Brockie, Ian
APPLICANT: Jenkins, Blizabeth
TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant Prot
CURRENT APPLICATION NUMBER: US/10/460,524
CURRENT FILING DATE: 2003-06-12
PRIOR APPLICATION NUMBER: US 60/388,059
PRIOR FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRY-YYTSDGTQGQTFWCDHAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 466.5; DB 30; Length
Pred. No. 6e-40;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 LLGNSYVDNTSKVTANFVKETASPTSTYDTYVE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LLGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 5, 2003, 20:25:13 Job time : 218.976 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Clostridium cellulovorans US-10-460-524-2
                                                                              RESULT 15
US-10-460-524-2
; Sequence 2, Application US/10460524
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.8%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 163
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2003, 20:13:32 ; Search time 14.5907 Seconds (without alignments) 824.821 Million cell updates/sec November Run on:

US-09-677-374-6 1335 1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

248976 segs, 47010500 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

1: /cgn2 6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2 6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2 6/ptcdata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2 6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2 6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2 6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2 6/ptcdata/2/paa/USO9_NEW_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		۵			SOUTHERNIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	1335	100.0	256	9	US-10-261-445B-6	Sequence 6, Appli
7	832	62.3	161	9	US-10-261-445B-4	4,
٣	815	61.0	162	9	US-10-241-602B-6	9
4	815	61.0	162	ø	US-10-261-445B-2	~
ß	245	18.4	599	'n	US-09-955-555B-29	Sequence 29, Appl
y	124	9.3	499	-	PCT-US03-19153-328	32
7	112	8.4	20	9	US-10-261-445B-16	16, 7
80	102.5	7.7	223	rv	US-09-581-286A-434	434,
6	102.5	7.7	230	Ŋ	US-09-581-286A-309	
10	94.5	7.1	106	'n	US-09-897-516A-5133	5133,
11	87	6.5	363	9	US-10-425-114A-61312	
12	86.5	6.5	66	9	US-10-389-647-605	
. 13	86.5	6.5	403	ഹ	US-09-897-516A-7766	1766,
14	86.5	6.5	1117	-	PCT-US03-21510-114	114, A
15	84	6.3	423	-	PCT/US02/39429-8	8, A
16	83.5	6.3	683	7	US-60-487-610-1870	
17	83.5	6.3	1397		PCT-US02-35624-174	
18	83	6.2	272	9	US-10-679-063-14893	1489
19	83	6.2	296	ø	US-10-425-114A-51273	Sequence 51273, A
20	83	6.2	345	9	US-10-425-114A-59685	
21	83	6.2	521	φ	US-10-425-114A-70443	Sequence 70443, A
22	83	6.2	3011	-	PCT-US03-19834-2	
23	82.5	6.2	497	ø	US-10-679-063-15782	1578
24	82.5	6.2	734	9	US-10-425-114A-49440	494
25	82.5	6.2	1327	Н	PCT-US03-28626-27	27,
56	82.5	6.2	1327	9	US-10-661-398-27	Sequence 27, Appl

	Sequence 22744, A Sequence 120, App Sequence 406, App Sequence 256, App Sequence 3444, Ap
US-09-674-546A-1669 US-10-679-063-23425 US-10-679-063-23425 PCT-USO3-28227-2863 US-60-478-196-3014 PCT-USO2-35624-95 US-10-009-002-5 US-10-425-114A-73075 US-10-689-006-24 US-10-689-006-24 PCT-USO2-39429-88 US-10-689-006-24 US-10-689-006-24 US-10-689-006-24 US-10-689-006-24 US-10-689-006-24 US-10-689-006-24 US-10-679-06-2745	US-10-679-063-22744 PCT-US03-19153-120 US-10-296-734-406 US-60-502-656-256 PCT-US03-26780-3444
.00171000001100	91971
2599 1261 1261 293 1016 3033 330 435 261 222 438	517 852 3011 2871 1755
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82.5 80.55 80.57 79.88 79.89 78.55 78.55	78 78 77 77
22200000000000000000000000000000000000	4 4 4 4 4 1 5 6 4 6

## ALIGNMENTS

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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRTNKQERRQQYCREFQQKAMIAGQKQEIYGT 240
                                                                                                                                                                                                                                                                                                                                                                                            1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQFFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGNSYVDNTSKVTANFVKETASPTSTYDDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS
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                                                                                                                                                                                                                                                                                                                               Length 256;
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 1335; DB 6;
100.0%; Pred. No. 1.5e-112;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 256; Conservative
                                                                                                                                                                                                                                                                           NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
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US-10-261-445B-6
                                                                                                                                                                                                                                LENGTH: 256
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241 ACPQPDGRWQVISTEK 256

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TYPE: PRT ORGANISM: Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-955-555B-29
                                               ; ORGANISM: F1:
US-10-241-602B-6
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  LENGTH: 162
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                                                                                                                                                                                      APPLICANT: NUZYK, MICHAEL A.

APPLICANT: RUZYK, MILIAM W.

APPLICANT: RAY, William W.

APPLICANT: Thornton, Julian C.

TILLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095

CURRENT APPLICATION NUMBER: US 09/677,374

PRIOR APPLICATION NUMBER: US 09/677,374

PRIOR APPLICATION NUMBER: US 60/154,437

PRIOR PELING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 4

LENGTH: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYKQE 120
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Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 161; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brouwers, Huub
APPLICANT: Jones, Simon
APPLICANT: Griffiths, Steve
APPLICANT: Valenzuela, Pablo
APPLICANT: Burzio, Luis
TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
FILE REFERENCE: H-32319A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
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CURRENT FILING DATE: 2002-09-11

PRIOR APPLICATION NUMBER: US/10/241,602B

CURRENT FILING DATE: 2002-09-11

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2000-03-11

PRIOR PLING DATE: 2000-03-11

PRIOR FILING DATE: 2000-07-01

PRIOR FILING DATE: 2000-07-01

PRIOR APPLICATION NUMBER: GB0016080.4

PRIOR FILING DATE: 2000-07-01

PRIOR APPLICATION NUMBER: GB001659.1

PRIOR FILING DATE: 2000-07-01

PRIOR FILING DATE: 2000-07-01

PRIOR FILING DATE: 2000-07-05

NUMBER: GEQ ID NOS: 34

SEQ ID NO 6
                                                                                                                             Sequence 4, Application US/10261445B
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
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GENERAL INFORMATION:
APPLICANT: Simard, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Piscirickettsia salmonis
241 ACPQPDGRWQVISTEK 256
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US-10-241-602B-6
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APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Ray, William W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64095
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR PAPLICATION NUMBER: US 06/154,437
PRIOR PLING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                      97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
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                                                                                                                                                                             62
                                                                                                                                                              RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
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   Length 162;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                        217 ROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 256
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Query Match 61.0%; Score 815; DB 6; L
Best Local Similarity 98.8%; Pred. No. 5.1e-66;
Matches 158; Conservative 1; Mismatches 1;
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GRNERAL INFORMATION:
APPLICANT: Bott, Richard R.
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Fowler, Timothy
APPLICANT: Liu, Chung-Cheng
APPLICANT: ward, Michael
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Query Match
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GENERAL INPORMATION:
APPLICANT: Diversa Corporation
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: WHETHOOS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-290W01
CURRENT APPLICATION NUMBER: PCT/US03/19153
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 378
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 328
LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                       TITLE OF INVENTION: Enzymatic Array and Process of Making TITLE OF INVENTION: Same TITLE OF INVENTION: Same TITLE OF INVENTION: Same CURRENT APPLICATION NUMBER: US/09/955,555B CURRENT PILING DATE: 2001-09-17 PRIOR APPLICATION NUMBER: US 60/005,701 PRIOR PILING DATE: 1995-11-17 PRIOR PILING DATE: 1995-11-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-17 PRIOR FILING DATE: 1995-10-1
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18.4%; Score 245; DB 5; Length 599;
Best Local Similarity 51.5%; Pred. No. 5.4e-14;
Matches 53; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.3%; Score 124; DB 1; Length 499;
Best Local Similarity 33.0%; Pred. No. 0.0033;
Matches 33; Conservative 14; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGN -- SYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Clostridium thermocellum
US-09-955-5558-29
Xia, Hai-Ying
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| LOCATION: (1) ...(29)
| PCT-US03-19153-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown
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    APPLICANT:
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: ASY, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US/10/261,445B
PRIOR PAPLICATION NUMBER: US 09/677,374
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PELICATION NUMBER: PCT/AU38/01023
PRIOR PELICATION NUMBER: PCT/AU38/01023
PRIOR PELING DATE: 1998-12-10
PRIOR PELING DATE: 1997-12-10
PRIOR PELING DATE: 1997-12-30
PRIOR PELING DATE: 1997-12-31
PRIOR PELING DATE: 1997-12-31
PRIOR PELING DATE: 1997-12-31
PRIOR PELING DATE: 1998-01-30
PRIOR PELING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: AU PP 2911
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-3
PRIOR PELING DATE: 1998-04-3
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-22
PRIOR PELING DATE: 1998-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 PVRTYQRYNKQERRQQYCRE 223
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ORGANISM: Porphyromonas gingivalis
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APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROTHEL, LINDA J.
MARGETTS, MAL B.
HOCKING, DIANNA M.
WEBB, ELIZABETH A.
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SEQ ID NO 434
LENGTH: 223
Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
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Query Match 7.1%;
Best Local Similarity 35.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                        Slater, Steven C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 363
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APPLICANT:
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                                                                                                                                     103 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 161
                                                                                                                                                                   103 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 161
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APPLICANT: MARGETTS, MAL B.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: WEBB, ELIZABETH A.
TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REFERENCE: 4137-3
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NUMBER OF SEQ ID NOS: 721
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                                             Length 223;
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                                                                                            Indels
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                                                 DB 5;
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                                        Ouery Match 7.7%; Score 102.5; DB Best Local Similarity 34.7%; Pred. No. 0.099; Matches 25; Conservative 13; Mismatches 3
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CURRENT FILING DATE: 2000-06-28
PRIOR PELING DATE: 1990-12-10
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
PRIOR PILING DATE: 1997-12-10
PRIOR PELING DATE: 1997-12-10
PRIOR PELING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: AU PP 1182
PRIOR APPLICATION NUMBER: AU PP 1846
PRIOR PILING DATE: 1998-01-31
PRIOR APPLICATION NUMBER: AU PP 2264
PRIOR PILING DATE: 1998-03-10
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-23
PRIOR PILING DATE: 1998-04-23
PRIOR PILING DATE: 1998-05-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: AU PP 3338
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
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US-09-581-286A-309
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: APTTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn version 3.2
                                                                                                                                                                                                                            162 SKIGQSMDQQDK 173
                                                                                                                                                                                                                                                       : ||: ||:| |
66 ALIGKKMDKQKK 77
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73 ALIGKKMDKOKK 84
US-09-581-286A-434
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RESULT 11
US-10-425-114A-61312
; Sequence 61312, Application US/10425114A
; Sequence 61312, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPRENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                               APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFRESENCE: 38-21(51847)8
CURRENT APPLICANN UNMERS: US/09/897,516A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.5%; Score 87; DB 6; Length 363; Best Local Similarity 26.8%; Pred. No. 4.6; Matches 38; Conservative 17; Mismatches 53; Indels
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US-10-425-114A-61312
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Pred. No. 0.2;
9; Mismatches
                                                          APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 5133
LENGTH: 106
; Sequence 5133, Application US/09897516A; GENERAL INFORMATION:
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6.5%; Score 86.5; Di
20.8%; Pred. No. 22;
cive 32; Mismatches
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Sequence 8, Application PC/TUS0239429
GENERAL INFORMATION:
APPLICANT: NeoRx Corporation
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Bearstyne, Erica A.
                                                                                                                                                                                                                                        PCT-US03-21510-114
; Sequence 114, Application PC/TUS0321510
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Conservative
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Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 DININDVKVRYYYTSDGTQGQTFWCDHAGALLGNSYVDNTSKVTANFVKETASPTSTYDT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph B.
APPLICANT: Huesing, Joseph B.
APPLICANT: Huesing, Joseph B.
APPLICANT: States, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Sprindonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REPERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 7766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.5%; Score 86.5; DB 6; Length 99; Best Local Similarity 34.3%; Pred. No. 0.95; Matches 24; Conservative 8; Mismatches 21; Indels
                                                                                                                                      Sequence 605, Application US/10389647
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: COSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7766, Application US/09897516A
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
146 RVSMAIGGAVLGGLIGSKIGQS 167
                                      94 AVAVAİĞAVVVDĞVAAPDLĞQA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i ORGANISM: Xenorhabdus sp. US-09-897-516A-7766
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EXO3-046C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21510
CURRENT FILING DATE: 2003-07-09
FRIOR PELICATION NUMBER: US 60/394,795
FRIOR FILING DATE: 2002-07-10
FRIOR FILING DATE: 2002-07-10
FRIOR FILING DATE: 2002-09-08-07
FRIOR FILING DATE: 2002-09-08-07
FRIOR FILING DATE: 2002-09-08-07
FRIOR FILING DATE: 2002-10-16
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63 DLSLKDPLMLAFFATVGLNANLASLRAGGKLL--LIFVVAVVGLLLVQNTVGIALAKML 119
                                                                                                                                  90 YLDPSHMRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFG-KGSGRVS 148
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                                                                                                                                                                                                                                                                            120 GLDP--LMGLLAG-----SVTLSG-----GHGTGAAWGKVFTERYGFENATEVA 161
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TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 69012-14701PC
CURRENT APPLICATION UNBER: PCT/US02/39429
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 413
TYPE: PRT
ORGANICM: Artificial Sequence
FRATURE:
FRATURE:
COTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gence
PCT/US02/39429-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 DPSHMRGCLQGSSLIIISVFLVGCAQ-----NFSRQEV-GAATGAVVGGVAGQLFGKGSG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.3%; Score 84; DB 1; Length 423; Best Local Similarity 25.2%; Pred. No. 10; Matches 55; Conservative 22; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 F--QQKAMIAGQKQEI----YGTACPQPDGRWQVISTE 255
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November 5, 2003, 20:06:21; Search time 29.3782 Seconds (without alignments) 875.264 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                 Copyright
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Perfect score:
                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                             Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•	de			SUMMARIES	
Result No.	Score	Query Match	o Query Match Length DB		di Oi	Description
	836	100.0	!	22	AAG78025	Piscirickettsia sa
7	836	100.0		22	AAB81126	OspA antigen amino
9	836			23	AAU97867	Piscirickettsia sa
4	815			22	AAB81127	Optimised OspA pro
Ŋ	815				AAU97868	Escherichia coli c
9	815.				AAB81128	C17E2 OspA constru
7	815	97.5	256	23	AAU97869	E. coli codon opti
ω	128.5	15.4			ABJ18820	Pseudomonas aerugi
σ	112	13.4		22	AAB81130	OspA B-cell epitop

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents P. salmonis OspA protein. An OspA protein with an Alternian and fusion partner is used in a vaccine to create an anti-OspA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia;
containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                              Length 162;
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 836; DB 22;
100.0%; Pred. No. 3.8e-80;
ative 0; Mismatches 0)
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                                       Example 2; Fig 2B; 35pp; English.
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(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                162 AA;
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BURIAN J.
                                                                                                                                                                                                                                                              antibody response
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                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                   The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                            New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
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; Pred. No. 3.8e-80;
0; Mismatches 0;
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/label= B_cell_epitope
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                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                      Claim 6; Fig 5; 25pp; English.
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Matches 162; Conservative
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         2001-639050/73.
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(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                   162 AA;
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                            N-PSDB; AAH79040.
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This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a pealmonis specific antigen termed 05pA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 1782. The DNA encoding OspA 1782 (Ar86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli codon optimised OspA, 17e2.
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                                                                                       Disclosure; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2000; 2000US-0677374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-455221/49.
N-PSDB; ABK52402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA2339327-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thornton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                      The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piecirickettsia Salmonis comprising administering either intraperitoneally, by immersion or oxally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicemia and other related this is the amino acid sequence of the Piscirickettsia salmonis outer wirtage in provide in outer surface lipoprotein, OspA, used in the creation of the vaccine described in the interval of the vaccine described in the interval of the vaccine described in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 836; DB 23;
100.0%; Pred. No. 3.8e-80;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimised OspA protein 17E2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= B_cell_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
109..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB81127 standard; Protein; 161 AA
  Claim 15; Fig 2; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CA-2281913
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-316844/34.
N-PSDB; AAF86247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW, Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                   162 AA;
                                                                                                                                                                                                                                                                                                        in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1999;
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121

Sequence

8X666666666668X8

AAB81127;

AAB8112

Synthetic

Region

(BURI/) | (KUZY/) |

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Gaps

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                                                                                         The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related immunity in fin-fish against Sickettsial septicaemia and other related This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLIGSKIGOSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96..256
/label= C17E2 OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                      Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...95
|Tabel= Undefined_N-terminal_fusion_partner
                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROOYCREFOOXAMIAGOKOEIYGTACROPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C17E2 OspA construct with N-terminal fusion partner.
                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 23;
Pred. No. 6.3e-78;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB81128 standard; Protein; 256 AA
                                                                 Example 4; Fig 5; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                        97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99CA-2281913
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.8
Matches 158; Conservative
                                 strain, as a vaccine
                                                                                                                                                                                                                                                                                                                          161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                           Sequence
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This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antiqen termed 05p4, or an immunogenic fragment of 0spA in the form of a vaccine. The method is used for protecting animals, particularly poixilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonis rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion patriner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGLIGSKIGQSMDQQDKIKINQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli codon optimised OspA, 17e2 with N-terminal fusion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROOYCREFOOKAMIAGOKOBIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 815; DB 22; 98.8%; Pred. No. 1.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97869 standard; Protein; 256 AA
                                                                                                                                                                                                    Example 4; Fig 5; 35pp; English
                                                  Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-2001; 2001CA-2339327.
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                                                  Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA;
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                    N-PSDB; AAF86248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                    Kay WW,
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modulating blofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating blofilm formation by bacteria. The method of the invention is acquaint bacterial antibiotic resistence. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; and medical device-associated infections, and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                         comprises a method for identifying a compound capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKI-----
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                                                                                                                                                                                                                      Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 128.5; DB 24; Length 182; 34.8%; Pred. No. 2.1e-05; tive 13; Mismatches 28; Indels 19;
                                                                   Greenberg EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 -KLNQSLEKV-----KAGQVTRWRNP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 161
                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 152; 154pp; English.
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                                                                      Lory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB81130 standard; Peptide; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99CA-2281913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 34.89 tes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piscirickettsia salmonis.
                                                                   Whiteley M, Bangera MG,
(HARD ) HARVARD COLLEGE.
                                                                                                                                  WPI: 2003-075601/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-316844/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAY W W.
BURIAN J.
                                                                                                                                                                 N-PSDB; ABT14642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAYW/) KAY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2281913-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2001
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(KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81130
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Pisciricketteia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer peptides lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (1722) with an N-terminal fusion used in the creation of the vaccine described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                        Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.5%; Score 815; DB 23; Length 256; 98.8%; Pred. No. 1.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                    Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                    Burian J,
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                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 5; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001US-285190P. 24-OCT-2001; 2001US-344142P.
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Matches 158; Conservative
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                                                                                                 Thornton JC, Kay WW,
                                                                                                                                                                                                                                                                                                                           strain, as a vaccine
                                                                                                                                                          WPI; 2002-455221/49.
N-PSDB; ABK52403.
                                    KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
   BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200285295-A2
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Best Local 9
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bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
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N-PSDB; AAL46497.
                                                                                                                                                                   Local Similarity
                                                                                   lipoprotein, OspA.
                                                                                                                  20 AA;
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29-AUG-2000;
29-AUG-2000;
01-SEP-2000;
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29-AUG-2000;
29-AUG-2000;
29-AUG-2000;
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                                                                                                                                                                                      50;
20;
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                                                                                                                    Sequence
                                                                                                                                                  Query Match
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                              This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed osph, or an immunogenic fragment of osph in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents an immunogenic epitope of the P. salmonis osph protein. The peptide is used to raise rabbit anti-Osph antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of protecting a polkilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial strain, as a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease.
   containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                      Score 112; DB 22;
Pred. No. 6.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer surface lipoprotein OspA based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burian J, Kuzyk MA;
                                                                                                                                                                                                                                                                                      ch 13.4%; Score 112; DE 1. Similarity 100.0%; Pred. No. 6.9
20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 17; 55pp; English.
                                    Example 2; Page 17; 35pp; English
                                                                                                                                                                                                                                                                                                                                                        110 PVRTYQRYNKQERRQQYCRE 129
                                                                                                                                                                                                                                                                                                                                                                                         1 PVRTYORYNKOERROOYCRE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU97871 standard; Peptide; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piscirickettsia salmonis.
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KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thornton JC, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUZYK M A.
                                                                                                                                                                                                                                                        20 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU97871;
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAYW/)
(BURI/)
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This sequence represents a synthetic peptide used to create polyclonal rabbit antibodies against the Piscirickettsia salmonis outer surface
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella, vaccine, respiratory tract infection, antiinflammatory, auditory; antibacterial; otitis media, sinusitis; pneumonia.
                                                                                                                                                                                                    ..
                                                                                                                                                            Length 20;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang Y;
                                                                                                                                                          Score 112; DB 23;
Pred. No. 6.9e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M catarrhalis MCA100414 protein SEQ ID NO: 10.
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                                                                                                                                            13.4%; Scor.
100.0%; Pred
0; F
                                                                                                                                                                                                                                           110 PVRTYQRYNKQERRQQYCRE 129
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                                                                                                                                                                                                                                                                                                                                                                                   AAO17565 standard; Protein; 197
                                                                                                                                                                                                                                                                      1 PVRTYQRYNKQERRQQYCRE
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2000US-229474P.
2000US-229475P.
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2000US-228443P.
2000US-228441P.
2000US-228442P.
2000US-228442P.
2000US-228442P.
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2000US-228742P.
2000US-228773P.
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2000US-228296P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVET ) AVENTIS PASTEUR LTD.
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis.
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29-NOV-2002
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                                                                                                                                                                                                                                                                                                              ABG80432;
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                                                                                        Sequence
                                                                                                             Query Match
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                                                                          The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce accines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                     29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                   8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG
                                                                                                                                                                                                                                        7 GVVLLASSMALAGCANTGT---TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB113 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a
                                                                                                                                                                                                                                                                             60 -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                      BASB311; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial.
                     immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                      12.9%; Score 108; DB 23; Length 197; 32.4%; Pred. No. 0.0033;
           Moraxella polypeptide and polynucleotides useful as vaccine
                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 67; 86pp; English.
                                                                                                                                                                                                                                                                                                                                              AAB20105 standard; Protein; 224
                                                     Claim 28; Fig 9; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0015044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-EP05851
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                 Local Similarity 32.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112458/12.
                                                                                                                                               197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200100836-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thonnard J;
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                     AAB20105;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyperblebbing, Gram-negative bacterium; genetically modified, Tol gene peptidoglycan-basociated site, outer-membrane; bacterial infection; vesicle-shedding; Bleb; filter sterilised; detergent; deoxycholate; homogeneity; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least lantibody directed against a BASB113 polypeptide. BASB113 polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AVLGGLIGSKIGQSMDQQDKIKLNQSLBKVKAGQVTRWRNPDTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| :|| :|| :|| EKTGRDAILGAAVGAAAGAYWERQAK----QIEQQWQGTGVTVTHDTDTGN
                                                                                                                                                                                                                                                                                                                                                                  Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Indels
                                                                                                                                                                                                                                                                                                                                                                  Score 108; DB 22;
Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TolQ; TolA; OmpCD; xOmpA; PAL-1; PAL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis PAL-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 71; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG80432 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neyt CA,
                                                                                                                                                                                                                                                                                                                                                                  12.9%;
32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2002; 2002WO-EP01361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              36, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berthet FJ, Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-657509/70.
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                 224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABS66202
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67 9

Gaps

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isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation be used to prophorymonas gingivalis in standard hybridisation especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
AAY34583, AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                                                 9 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAM-AIGGAVLGGLIG
                                                                                                                                                                                                         ASVLAVALVFAGCGLN--NMAKGGLIGAGVGGAIGAGVGNVAGNTAVGAIVGTAVGGAAG
                                                                                                                              Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                          gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphorymonas gingivalis peptides for preventing
                                                                                                                     Score 105.5; DB 20; Leus----
Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margetts MB,
                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 325-326; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis protein PG3
                                                                                                                                                                                                                                                                                                                          AAY34362 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hocking DN
Webb EA;
                                                                                                                               12.6%;
36.1%;
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98AU-0001546.
98AU-0002264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0000839
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                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                         26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphorymonas gingivalis.
                                                                                                                                                                                                                                   79
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ALIGKKMDKOKK
                                                                                                                                                                                                                                   SKIGOSMDOODK
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-385613/32
                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphorymonas ging
vaccine; antigenic
                                                                                                       223 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9929870-A1
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05-MAY-1998;
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25-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1998
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30-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic P
gingivitis
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                                                                                                                                                                                                                                                                                                                                                  AAY34362;
                                                                                                                                                                                                                                     68
                                                                                                       Sequence
                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agius
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              the use of detergents such as deoxycholate, thus obviating chromatography purification and ultra centrifugation steps. Vesicles prepared from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present amino acid sequence represents a Moraxella catarrhalis protein, as described in the invention.
                                                                                                                                                                                 8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG 59
                                                                                                                                                                                                          GVVLLASSMALAGCANTGT --- TGNGTGFGGANVNKAVIGAVAGAL --- GGTAISKATGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
  The blebs can be made and harvested without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 (
AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                  |:|| :|: | :|| :|| | EXTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                   60 -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 104
                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                          periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patterson MA;
                                                                                                                           ch 12.9%; Score 108; DB 23; Length 224; 1 Similarity 32.4%; Pred. No. 0.0039; 36; Conservative 16; Mismatches 35; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MΒ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis protein PG3
                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 469; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                          AAY34487 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas gingivalis; PG; vaccine; antigenic.
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98AU-0001546.
98AU-0002264.
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 filter sterilised.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphorymonas gingivalis
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Rothel LJ,
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                                                                                                                             Query Match
Best Local Similarity
                                                                                                      224 AA;
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30-JUL-1998;
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05-MAY-1998;
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gingivitis
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                                                                                                       Sequence
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AAY34487
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cc isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be cc used as vaccines especially against Porphorymonas gingivalis. Probes can cc used as vaccines especially against Porphorymonas gingivalis in standard hybridisation cc assays. Porphorymonas gingivalis is involved in periodontal disease cc cypecially gingivitis.

CC (Updated on 20-MAR-2003 to correct PR field.)

XX Sequence 230 AA;
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	2;	67	72
	Gaps	regrie	VGGAAG
230;	3;	AIGGAV	AIVGTA
Length	31; Indels 3; Gaps	SSGRVAM-	VAGNTAVG
DB 20;	31;	AGOLFGK	IGAGVGN
12.6%; Score 105.5; DB 20; Length 230; 36.1%; Pred No 0 0074.	smatches	TGAVVGGV	IGAGVGGA
Score	12; Mi	RQEVGAA	NMAKGGL
	~	9 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAM-AIGGAVLGGLIG 67	15 ASVLAVALVFAGCGINNMAKGGLIGAGVGGAIGAGVGNVAGNTAVGAIVGTAVGGAAG 72
Query Match Best Local Similarity	Conserv	LIIISVFL	ASVLAVALVE
tch al Sim	26;	S 6	15 AE
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Oy 68 SKIGOSMDOODK 79 : ||:||:||:| Db 73 ALIGKKMDKQKK 84

Search completed: November 5, 2003, 20:12:49 Job time : 30.3782 secs

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1 MNRGCLQGSSLIIISVFLVG......IYGTACRQPDGRWQVISTEK 162
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 8, Appli Sequence 7100, Ap Sequence 2, Appli Sequence 2, Appli Sequence 19162, Ap Sequence 19162, A Sequence 21525, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2348, Appli Sequence 6584, Appli Sequence 6584, Appli	D SEQUENCES RELATING TO PSEUDOMONAS AND THERAPEUTICS	Length 192; Indels 19; Gaps 2; KIGQSMDQQDKI 80  ::  KVQEGMQERDTYTTETRC 139	UENCES RELATING TO PSEUDOMONAS THERAPEUTICS
4 US-09-618-869-8 4 US-09-328-352-1100 2 US-09-067-351-2 3 US-09-360-490-2 4 US-09-328-352-5775 4 US-09-252-991A-19162 4 US-09-252-991A-26438 3 US-08-374-077C-2 3 US-08-374-077C-2 4 US-09-539-879-2 4 US-09-539-879-2 1 US-08-440-519-12 4 US-09-107-532A-4748 4 US-09-107-532A-4748 4 US-09-107-532A-4748	is	4%; Score 128.5; DB 4; 13; Pred. No. 1.3e-06; 13; Mismatches 28; GQLFGKGSGRVAMAIGGAVLGGLIGS                   GNQIGGGTGKKIATVAGAVGGGYAGNKAGQVTRWRNP 100                 KYMLDGKAGQIRMERPP 171	cation US/09252991A  Rubenfield et al.  NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 1196.136 1199-02-18 MNBER: US 60/074,788 11998-02-18 MMBER: US 60/094,190
77.5 9.3 255 77 9.2 141 77 9.2 551 76.5 9.2 558 76.5 9.2 258 76.5 9.2 258 76.5 9.2 258 76.5 9.2 2516 76.5 9.2 2516 76.5 9.2 2516 76.5 9.2 2516 76.5 9.1 1021 76 9.1 1021 76 9.1 1021 76 9.1 1021 76 9.1 1021 77 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021 78 9.1 1021	1 252-991A-22817 ence 22817, Appli nt No. 6551795 tic Nor Inversion: LE OF INVENTION: LE OF INVENTION: LE OF INVENTION: RENT APPLICATION RENT APPLICATION RENT FILING DATE: OR APPLICATION NU OR FILING DATE: OR PILING DATE: OR PILING DATE: OR PILING DATE: PER OF SEQ ID NOS RIUNG DATE: PER OF SEQ ID NOS RIUNG DATE: RENT PRI NO 22817 GANISM: PSEUGGMOON 252-991A-22817	Match Local S es 32 28 80 81	SULT 2 -09-252-991A-19701 Sequence 19701, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: ARRUGINOSA FOR DIAGRATITE OF INVENTION: ARRUGINOSA FOR DIAGRATICE TO THE REFERENCE: 107196-136 CURRENT APPLICATION NUMBER: US/09/252,991 CURRENT FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18
	RESULT US-09-1 Sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the	Query Best Match Oy Db Oy Oy	RESULT OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND

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Sequence 8009, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR PAPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1999-02-18 PRIOR FILING DATE: 1999-02-18 PRIOR FILING DATE: 1999-07-18 PRIOR FILING DATE: 1999-07-27 SEQ ID NOS: 33142 SEQ ID NOS: 33142 SEQ ID NOS: 33142 LENGTH: 387
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABCUGIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 98.5; DB 4; Length 387; llarity 22.1%; Pred. No. 0.0073; Conservative 26; Mismatches 47; Indels 61
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Matches 38; Conserv
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US-09-252-991A-23334
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; Sequence 21754, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR PELLING DATE: 1999-02-18
; PRIOR PELLING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; BLENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                             91 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ---ERRQQYCREFQOKAMIAGQKQEIYGTA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 IG-----SYGTDVDRSTVEINRSVAYAKSAÓSCYQSÓFKÁLLDGRKNK----S 171
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                                                                                                                                                                                           Query Match 13.9%; Score 116; DB 4; Length 165; Best Local Similarity 25.0%; Pred. No. 2.6e-05; Matches 34; Conservative 21; Mismatches 41; Indels
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1 Similarity 23.5%; Pred. No. 0.0025;
44; Conservative 29; Mismatches 49;
                                                                                                                                                                                                                                                                                                1 MNRGCLOGSSLIIISVFLVGC----AQNFSRQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 STRAYVQQVDQGQIFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , APPLICANT: Marc J. Rubenfield
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Best Local Similarity
Matches 44; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 CRQPDGR 154
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                  NUMBER OF SEQ ID NOS:
SEQ ID NO 19701
LENGTH: 165
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                                                                                                                     ORGANISM: Pseudor
US-09-252-991A-19701
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Sequence 4253, Application US/09328352

Sequence 4253, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4442
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                                                                                                                                                             64 MNEG---GENLVATGAGTLG-----GAAVGAAFGVVGGP-----PGAVVGGIIGG 105
                                                                                                                                                                                                                     61 VLGGLIGSKIGQSMDQODKIKLNQSLEKVKAGQVTRWRNPDT--GNSYSVEPVRTYQRYN 118
                                                                                                                                                                                                                                                               -----DSNDWQEEDNYWRENYKKMP-----YY 145
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                                                                                                                                  1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GSSLIIISVFLVGCAQ-----AVVGGVAGQ
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                                                                                        Gaps
                                                                                     41;
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                                            Length 215;
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                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                   52;
                                       Score 87.5; DB 4;
Pred. No. 0.057;
1; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 85.5; DB 4; 22.0%; Pred. No. 0.48; tive 30; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRNPDTGNSY-SVEPVRTYQRYNKQERRQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 WKLKVPSSSFNSTQQIDVKAGYALÓDQQAE 475
                                                                                                                                                                                                                                                                                                             119 KOERROOYCREFQOKAMIAGOKOEIYGTA 147
                                                                                                                                                                                                                                                                                                                                       146 SEDKNLEYDRDY-RAAYRLGYENRVHNNA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4442, Application US/09328352
Patent No. 6562958
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US-09-328-352-4442
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                                                                                     21;
                                         10.5%;
23.5%;
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                                                                                     Conservative
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                  Query Match
Best Local Similarity
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US-09-328-352-6750
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Batent No. 6562958

GENERAL INFORMATION:
APPLICAMY: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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APPLICANT: Gary L. Breton et al.

APPLICANT: Gary L. Breton et al.

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: BADMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 PLILGWVQQQGGLQAALEKLKGAGLGSQVQSWVDPNQSN--SEVPTQQLQSLFNPADIEQ 144
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                                                                                                                                                                                                                                                                                                                  32 GCMLGSVLGÓMGGNTS---SGAQGG--LGGVLGSVLGQVTGNNNTPQTGGGVQSLLIAVV 86
                                                                                                                                                                                                                                                                                      9 SSLIIISVFLVGCAQNF--SRQEVGAATGAVVGGVAGQLFGKGSGR-VAMAIGGAV----
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20;
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                                                                                                                                                                                              Query Match 10.8%; Score 90; DB 4; Length 126; Best Local Similarity 31.8%; Pred. No. 0.015; Matches 27; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.6%; Score 89; DB 4; Length 199; Best Local Similarity 25.7%; Pred. No. 0.035; Matches 36; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 GAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQ---
CURRENT APPLICATION NUMBER: US/09/328,352
                                                                                                                                                                                                                                                                                                                                                                                                        :| | | | :::
77 QGGSKQTTTKSAIGAGIGSVVGKAI 101
                                                                                                                                                                                                                                                                                                                                                                              ---LGGLIGSKIGQSM 74
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Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 VAQQAQ-----APKEQVYG 158
                                                                                                        TYPE: PRT CORGANISM: ORGANISM: Acinetobacter baumannii US-09-328-352-8009
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US-09-328-352-7802
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                  CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8009
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LENGTH: 215
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                                                                                     LENGTH: 126
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Sequence 7068, Application US/09328352

Sequence 7068, Application US/09328352

Batent No. 5562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7068
                                                                                                                                                                                                                                                                                      PARENTE NO. 3331/33.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOS POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1999-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 -----RVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAG----QVTRWRNP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GLILGGFAGE-----SLVGALLGGLSGLALGQAVSLQNLAQQNERLRKQMSEFA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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25.2%; Pred. No. 0.27;
tive 20; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 TRWRNPDTGNSYSVEPVRTYQRYNKQBRRQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 82; 27.5%; Pred. No.
22 AQNFSRQEVGAATGAVVGGVAGQLFGK--
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa US-09-252-991A-33036
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Best Local Similarity 25.2%
Matches 36; Conservative
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Best Local Similarity 27.5%
Matches 25; Conservative
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i Sequence 28337, Application US/09252991A

j Sequence 28337, Application US/09252991A

j Patent No. 6551795

j GABERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28397

LENGTH: 127
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Factor 10. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26658
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10.0%; Score 83.5; DB 4; Length 127;
Best Local Similarity 32.9%; Pred. No. 0.079;
Matches 23; Conservative 9; Mismatches 21; Indels 1'
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                            24; Indels
       29.7%; Pred. No. 0.14;
                                 Mismatches
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       Best Local Similarity
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RESULT 15

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US-08-556-978B-19

US-08-556-978B-19

SEQUENCES: Application US/08556978B

SERVER 100 NUMBER OF SEQUENCES: 100

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TITLE OF INVERTION: SIDE SILK ANALOGS

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDERSS: 107

COURTY: UNITED STATES OF AMERICA

TITLE OF INVERTION STATES OF AMERICA

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COUNTRY READABLE FORM:

MEDILIN TYPE: 1999B

FILLING DAME: UNITED STATES OF AMERICA

COMPUTER READABLE FORM:

MEDILIN TYPE: 015867712 3.50 INCH

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ALIGNMENTS

14378, A 5811, Ap 8, Appli 8, Appli 8, Appli

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2 US-09-861-331-1

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3 US-09-981-33-19

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US-10-261-446-2
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Sequence 1, Appli Sequence 1, Appli Sequence 341, App Sequence 19, Appl

Sequence 101, App Sequence 21, Appl Sequence 1381, Ap Sequence 33055, A Sequence 8774, Ap

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Sequence 16, Application US/10261446
Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: Ruzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Thornton, Jan
APPLICANT: Thornton, Juliam V.
APPLICANT: Thornton, Juliam C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
                                                                                                                                                                                                                                       GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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SEQUENCE 169, Application No. US20030113742A1

SEQUENCE INFORMATION:

APPLICANT: Whiteley, Marvin

APPLICANT: Bangera, M. Gita

APPLICANT: Brangera, M. Gita

APPLICANT: Greenberg, Everett Peter

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF TITLE OF INVENTION: BIOFILM FORMATION

FILE REFERENCE: UIZ-070CP

CURRENT APPLICATION NUMBER: US/10/127,032

CURRENT FILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 170

SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                  Length 256;
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                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                     123 ROOYCREFOOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 256
                                                                                                97.5%; Score 815; DB 12;
98.8%; Pred. No. 3.5e-77;
tive 1; Mismatches 1;
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                                                                                                                          Best Local Similarity 98.8
Matches 158; Conservative
                         (-92) .. (-1)
  NAME/KEY: SIGNAL
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                                                                                                  Query Match
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCIDES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE REPERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US, 10/261,446
CURRENT PILING DATE: 2002-09-30
PRIOR PRIOR APPLICATION NUMBER: US 60/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
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                               121 ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
121 ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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Pred. No. 1.9e-77;
1; Mismatches 1;
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ORGANISM: Piscirickettsia salmonis
PEATURE:
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                                                                                                                                                                      ; Sequence 4, Application US/10261446; Publication No. US2030165526A1; GENERAL INFORMATION: APPLICANT: KUZYK, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10261446
Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
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Best Local Similarity 98.8%;
Matches 158; Conservative
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LENGTH: 161
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LENGTH: 256
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US-10-261-446-4
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US-10-261-446-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 ÓGAGAAAAAVGAGQEGIRGÓGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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TITLE OF INVENTION: Production of Silk-Like Proteins in Plants
FILE REPERENCE: BC1014 US NA
CURRENT APPLICATION NUMBER: US/10/414,760
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US/09/863,859
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/206968
PRIOR PILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                           Length 651;
                                                                                                                                                                                                                                                                                                                                   17; Indels
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Pred. No. 6.7;
3; Mismatches
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9.7%; Score 81.5; DE
Best Local Similarity 36.8%; Pred. No. 6.7;
Matches 25; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 341, Application US/09864864;
Patent No. US70020102679A1
GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Scrist, Heather
APPLICANT: Lodes, Michael J.
APPLICANT: Algate, Paul A.
                  PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: PR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO I
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US-10-414-760-1
'Sequence 1, Application US/10414760
'Publication No. US20030192077A1
'GENERAL INFORMATION:
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  2001-05-22
                                                                                                                                                                                                                                                                                         Query Match
9.7%;
Best Local Similarity 36.8%;
Matches 25; Conservative
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SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENCTH: 651
                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Nephila clavipes
US-09-861-597-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Nephila clavipes US-10-414-760-1
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US-09-864-864-341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10091724
; Sequence 5, Application US/20030105310A1
; Publication No. US20030105310A1
; GENERAL INFORMATION:
    APPLICANT: Children's Medical Center Corporation
    APPLICANT: Ashkar. Samy
; TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
; TITLE OF INVENTION NUMBER: US/10/091,724
; CURRENT APPLICATION NUMBER: US 60/306,946
; PRIOR APPLICATION NUMBER: US 60/306,946
; PRIOR FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 53
; SSQ ID NO 5
; SEQ ID NO 5
; LENGTH: 71
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PEDLICANT: ARRADBAU, Jean-Pierre

TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT

TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN

TITLE OF INVENTION: AMALOG

FILE REFERENCE: 6388-0365-0

CURRENT APPLICATION NUMBER: US/09/861,597
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                                                                                                                                                                                                                                                                                    Query Match
13.4%; Score 112; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 20; Conservative 0; Mismatches 0;
                  PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                             110 PVRIYORYNKQERRQQYCRE 129
                                                                                                                                                                                                                                                                                                                                                                                                                         1 PVRTYORYNKOERROOYCRE 20
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Patent No. US20020064539A1
GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GLIGSKI 70
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65 AVLGGQI 71
FILING DATE:
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                                                                                                                                                    SEQ ID NO 16
LENGTH: 20
CURRENT
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APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon A.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
Protein Kinase Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 VQAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRTGAIVDVPVGE---EL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 SGRVAMAIGGAVLG-GLIGSK------IGQSMDQQDKIKLNQSLEKVKAGQ 93
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                      Length 553;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 ----RELIIGDRQTGKTSIAIDTIINQKRFNDGSDEKKKLYC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 VTRWR-----NPDIG-NSYSVEPVRIYORYN--KOERROOYC 127
                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                   Query Match
9.5%; Score 79.5; Di
Best Local Similarity 25.3%; Pred. No. 8.7;
Matches 41; Conservative 20; Mismatches
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CURRENT APPLICATION NUMBER: US/10/17,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2002-09-25
PRIOR PILING DATE: 2002-09-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-14
NUMBER: OF SEQ ID NOS: 506
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                   6 LOGSSLIIISVFLVGCAQNFSRQEVGAA----
                                             FILE REFERENCE: P-NI 3906
CURRENT APPLICATION NUMBER: US/09/738,630
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/10177293
Publication No. US20030124128A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bast Jr., Robert C.
Hortobagyi, Gabriel D
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myer, Vic
Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lillie, James APPLICANT: Glatt, Karen
                                                                                                                                                                                                                           tYPE: PRT
CORGANISM: Homo sapiens
US-09-738-630-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, Xumei
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 LGRVVDALGNAIDGKGPIGSKTRRRVGLKAPGIIPRISVREPMOTGIKAVDSLVPIGRGO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TGAVVGGVAGQLFGKG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 SGRVAMAIGGAVLG-GLIGSK-----IGQSMDQQDKIKLNQSLEKVKAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 GALIGGMVGGPIGLLAGFKVAGIAAALGGGVL-GFTGGKLIQRKKQKMMEKLTSS 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQS
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1
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 553;
                                                                           APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REPERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SEQ ID NOS: 341
SEQ ID NO 341
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020160382A1 3040213CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 101, Application US/09738630
Publication No. US20030166213A1
GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
APPLICANT: Shaw, Paul J.
TITLE OF INVENTION: Mehtods For Identifying Compounds That
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTRWR-----KQERRQQYC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICAMT: Lasek, Amy W.
; APPLICAMT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION UNDER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 80.5; DB 10;
41.8%; Pred. No. 3.1;
tive 5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.5%; Score 79.5; DB 10;
Best Local Similarity 25.3%; Pred. No. 8.7;
Matches 41; Conservative 20; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LQGSSLIIISVFLVGCAQNFSRQEVGAA---
                                Mannion, Jane
Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.6
Best Local Similarity 41.8
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-864-864-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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US-09-981-353-19
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LENGTH: 553
TYPE: PRT
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                                APPLICANT:
APPLICANT:
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31; Conservative
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 APPLICANT: Penn, Sharron G.
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                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               US-10-029-386-33055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-8774
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                                                                                                                                                      SEQ ID NO 33055
LENGTH: 208
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APPLICANT: H
APPLICANT: S
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                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                 147 LGRVVDALGNAIDGKGPIGSKTRRRVGLKAPGIIPRISVREPMOTGIKAVDSLVPIGRGO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (562)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1381
                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                         ----TGAVVGGVAGQLFGKG 49
                                                                                                                                                                                                     ---IGOSMDQQDKIKLNQSLEKVKAGQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 NFSRQEVGAATGAVVGG--VAGQLFGKGS----GRVAMAIGGAVLGGLIGSKIGQSMDQQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 DKI-----KLNQSLEKVKA-----GQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                        Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.4%; Score 79; DB 10; Length 618;
Best Local Similarity 28.0%; Pred. No. 11;
Matches 33; Conservative 13; Mismatches 46; Indels 26; Gaps
                                                                           Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                 ----RELIIGDRQTGKTSIAIDTIINQKRFNDGSDEKKKLYC 244
                                                                                                                                                                                                                                                                94 VTRWR-----NPDTG-NSYSVEPVRTYQRYN--KQERRQQYC 127
                                                                           DB 15;
                                                                                                        54;
                                                                         Query Match
9.5%; Score 79.5; D
Best Local Similarity 25.3%; Pred. No. 8.7;
Matches 41; Conservative 20; Mismatches
                                                                                                                                     6 LQGSSLIIISVFLVGCAQNFSRQEVGAA----
                                                                                                                                                                                                  50 SGRVAMAIGGAVLG-GLIGSK-----
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; Sequence 33055, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1381, Application US/09925300 Patent No. US20020151681A1
             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-925-300-1381
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LENGTH: 618
LENGTH: 553
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APPLICANT: Rank, David R.
APPLICANT: Harzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GGGTGGGGGGTGGGGGGTGGGGGGGGGGGGGTVGLPQGVPGGGQDSTALKQTRRPAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 VKAGOV-----TRWRNPDTGNSYS------VEPVRTYQ----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK
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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO ACO11553.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                     FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AGOVTRWRNPDTGNSYSVEPVRTYQRYNKQE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 A-RVIR----PIGRIQ--QPLRSSPRHARED 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-27697
PRIOR FILING DATE: 2001-05-30
PRIOR APLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8774, Application US/10156761
Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISHIKAWA, JUN
HORIKAWA, HIROSHI
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409 LQAGDLLLLHTDGLVPRRWADPRSSEAESGGGTAAVQRLLDLAPRFDGVRTAQHCVRTVV 468

116 -RYNKQERRQQYC 127 : | | | 469 EEFGETEREDDAC 481

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Search completed: November 5, 2003, 20:27:19 Job time : 20.0259 secs

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

November 5, 2003, 20:10:11; Search time 11.4715 Seconds (without alignments) 1358.089 Million cell updates/sec Run on:

US-09-677-374-2 Perfect score:

1 MNRGCLQGSSLIIISVFLVG......IYGTACRQPDGRWQVISTEK 162 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	rickettsial common	Rickettsial common	Rickettsial common	17K surface antige		17K antigen precur		17K surface antige	conserved hypothet	outer membrane lip	rved hypot	lipa protein [impo	protein	protein	heti	0		outer	probable outer mem	outer membrane lip	outer membrane lip	-react	probable secreted	outer membrane pro	hypothetical prote		hypothetical prote		probable outer mem
	aı	D33971	B33971	A33971	G97860	C33971	A25972	D83169	AI3418	B83514	S23787	B82837	AD2696	D97478	S58234	G87629	AF0289	C64921	F90922	B85771	AI0693	AG0443	I64130	AE0644	AD3350	H83636	D85674	H90814	C64855	G91049
	DB	~	~	~	~	~	N	N	N	N	~	7	~	7	N	~	~	~	N	~	~	~	~	7	~	~	~	~	~	7
	Length	159	159	159	159	159	159	182	131	154	155	257	142	125	139	232	155	155	155	155	155	155	155	179	232	Ó	179	179	179	172
ouerv	Match	35.4	35.0	35.0	35.0	34.0	34.0	15.4	15.0	13.9	13.6	13.4	13.3	13.3	13.3	13.2	13.0	12.6	12.6	12.6	12.6	•	12.2	12.2	12.2	12.1		•	11.8	11.7
	Score	296	293	293	293	284.5	284	128.5	125.5	116	113.5	112	111.5	111	111	110.5	108.5	105.5	105.5	05.	105.5	104	102	102	102	101.5	66	66	66	98
Result	NO.	н	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

B33971 Rickettsial common antigen precursor - Rickettsia conorii

RESULT 2

probable outer mem	hypothetical prote	probable exported	probable lipoprote	hypothetical prote	hypothetical prote	glycine-rich prote	hypothetical prote	hypothetical prote	conserved hypothet	keratin, 54K type	PBSX prophage ORF	porin [imported] -	probable outer mem	probable tape meas	hypothetical prote
D85894	H65026	AC0198	C82230	AB3091	H98195	T05442	F87413	G97672	AE2897	KRBOVI	F69732	AI2910	G97685	F91251	B82998
~	~	~	7	7	~	N	~	N	~	н	~	~	~	7	N
172	172	179	223	278	278	608	257	100	100	526	1332	220	220	691	137
11.7	11.7	11.7	11.5	11.2	11.2	11.2	11.2	11.0	11.0	10.8	10.8	10.7	10.7	10.7	10.6
98	98	96	96	94	94	94	93.5	92	92	90	90	89.5	89.5	89.5	88

## ALIGNMENTS

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rickettsial common antigen precursor - Rickettsia prowazekii
N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Accession: D33971; B71645
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference numbor: A33971; MUID:89359171; PMID:2768201
A;Reference numbor: A33971; MUID:89359171; PMID:2768201
A;Residues: preliminary
A;Residues: DNA
A;Residues: L-159 <AND>A;Residues: Comparative equence in GenBank entry RIRANTITKC, release 109.0, (PID:9152462) omits the R;Anderson. S.G. E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, I.
Nature 396, 133-140, 1998
A;Recession: B71645
A;Recession: B71645
A;Recession: B71645
A;Recession: B71645
A;Recession: B71645
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A;Recession: B71645
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A;Residues: 1-159 <ANZ>
A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15258.1; PID:g386135
A;Experimental source: strain Madrid E
C;Genetics:
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C,Superfamily: rickettsial common antigen
C,Keywords: surface antigen
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
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C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Accession: A33971
J: Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene. A;Reference number: A33971, MUID:89359171; PMID:2768201
A;Accession: A33971
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-159 <AND>
A;Residues: 1-159 <AND>
A;Cross-references: GB:M28480; NID:9152457; PIDN:AAA26376.1; PID:9152458
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: G97860
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
               CjDate: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
CjAccession: B3371
RjAnderson, B.B.; Tzianabos, T.
RjAnderson, 171, 5199-5201, 1989
A,Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A,Reference number: A33971, MUID:89359171; PMID:2768201
A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-159 <AND>
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17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsial common antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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Best Local Similarity 38.1%; Pred. No. 1.2e-18;
Matches 61; Conservative 29; Mismatches 56;
                                                                                                                                                                                                                                                                                                   Query Match 35.0%; Score 293; DB 2; Best Local Similarity 38.1%; Pred. No. 1.2e-18; Matches 61; Conservative 29; Mismatches 56
Species: Rickettsia conorii
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17K antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
C;Accession: A25972 R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E. J. Bacteriol. 169, 2385-2390, 1987
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii
A;Recession: A25972
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V. Bacteriol. 171, 5199-5201, 1989
A,Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A,Reference number: A33971; MUID:89359171; PMID:2768201
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: G97860 A;Accession: G97860 A;Atatus: preliminary A;Molecule type: DNA A;Residues: 1-159 <KUR> A;Coss-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173 C;Genetics: A;Gene : omp C;Superfamily: rickettsial common antigen
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C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsial common antigen precursor - Rickettsia typhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%; Score 293; DB 2; 38.1%; Pred. No. 1.2e-18; iive 29; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 284.5; DB 2
Pred. No. 6.8e-18;
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39.3%; Pred. No. b.c.
ive 25; Mismatches
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CjAccession: B83514
RjStover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathr A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04442.1; GSPDB:GN001
A;Experimental source: strain PAO1
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523787
outer membrane lipoprotein precursor - Yersinia enterocolitica
cuter membrane lipoprotein precursor - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C;Accession: S23787
R;Baeumler, A.J.; Hantke, K.
J. Bacteriol. 174, 1029-1035, 1992
A;Title: A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Esr
A;Accession: S23787
A;Accession: S23787
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IGSIAGAGVGGVAGSAVGGGKGSYVAAIIGAVAGGLLGAATEEGLTRTQGVEITVREDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: "Freudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GKGSG--FPSLGGSSQKPETNLLASLGNGLFGNSASQLSAADRRKALBAEYRALEYSPAG
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                                                                                                                                                                                                                                                                                                                                                                                       47 GKGSGRVAMAIGG------AVLG-GLIGSKIGQ--SMDQQDKIKLN-QSLEKVKAG
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                                                                                                                                                                                                                   Length 131;
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                          ; Score 125.5; DB 2;
; Pred. No. 0.00052;
18; Mismatches 43;
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C;Superfamily: PAL cross-reacting lipoprotein
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A;Experimental source: strain 16M C;Genetics: A;Gene: BME11335 A;Map position: I
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Best Local Similarity 31.7%;
Matches 39; Conservative 1
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Best Local S:
Matches 34
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C;Species: Pseudomonas aeruginosa
C;Date: 15-59p-2000 #sequence_revision 15-5ep-2000 #text_change 01-Mar-2002
C;Accession: D83169
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor
A;Recence number: A82950; MUID:20437337; PMID:10984043
A;Recence number: A82950; MUID:20437337; PMID:10984043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <STO>
A;Cross-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07206.1; GSPDB:GN001
A;Cross-references: strain PA01
C;Genetics:
A;Gene: PA3819
C;Superfamily: PAL cross-reacting lipoprotein
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein PA3819 [imported] - Pseudomonas aeruginosa (c
C;Specise: Pseudomonas aeruginosa
C;Date: 15-Sep.2000 #sequence_revision 15-Sep-2000 #text_change 01-Mar-2002
C;Accession: D83169
                                                                                                                                                                                                                                                                                                                                                                                       9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                           28 QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKI-----
                                                                                                                                                                                                               Query Match 34.0%; Score 284; DB 2; Length 159;
Best Local Similarity 37.5%; Pred. No. 7.5e-18;
Matches 60; Conservative 29; Mismatches 57; Indels 14; Gaps
                                               A;Residues: 1-159 <AND>
A;Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 RNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KAGQVTRWRNP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <KUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: AI3418
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Matches
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LipA protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97478
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Residues: 1-125 «KIR»
                                 Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                       ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                               A;Residues: 1-142 «KUR»
A;Cross-references: GB:AE008688; PIDN:AAL41986.1; PID:g17739358; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 LETAPVGTPVIWTGDDVKGQVVANAP---YQVGN-----QNCRQYSHTLTVDGRDTRVR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 LEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 IGQSMDQQDKIKL----NQSLEKVKAGQVTRWRNPDT-GNSYSVBPVRTYQRYNKQERRQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE007869; PIDN: AAK86781.1; PID: g15155981; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 SILCVSM-LSAC-----TITGTRPAG--GSLFGR-SAQPSTPFLANLQGGIVG-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LSACTITGTRPAGGSLFGR-SAQPSTPFLANLQGGIVG-KSGVELDRGDQTKALEAEFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL----NQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.3%; Score 111.5; DB 2; Best Local Similarity 27.2%; Pred. No. 0.0095; Matches 41; Conservative 21; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.5%; Pred. No. 0.0092;
Matches 36; Conservative 18; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 ONCROYSHTLTVDGRDTRVRGAACRNDDGSW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYCREFQQKAMIAGQKQEIYGTACRQPDGRW 155
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S58234
lipA protein - Rhizobium leguminosarum
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: lipA
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: AGR C 1782
A;Map position: circular chromosome
P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GTACROPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACRNDDGSW 121
                                                                                                                                                                                                              A;Accession: AD2696
A;Status: preliminary
A;Molecule type: DNA
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Notes: For a complete list of authors see reference number A59328 below
A;Reference number: B82837
A;Accession: B82837
A;Accession: B82837
A;Residues: 1-257 <21M>A;Residues: 1-257 <21M>A;Residues: D;A;Accession: B82837
A;Residues: J-257 <21M>A;Residues: C;A;Accession: B82837
A;Residues: J-257 <21M>A;Residues: C;A;Accession: B828091.1; GSPDB:GN001
A;Residues: D;A;Coss-references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN001
A;Residues: J-257 <21M>A;Residues: C;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;A;Accession: Ba;Accession: Ba;A
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VGAAT 34
                                                                                                                                                                                                                                                                                                                                                                                            7 AVAİAAVTLIGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein XP0178 [imported] - Xylella fastidiosa (strai
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                       51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                      A;Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                             Length 155;
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Pred. No. 0.016;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                43;
                                                                                                                                                                                 DB 2;
                                                                                                                                                                          Query Match 13.6%; Score 113.5; DB Best Local Similarity 24.7%; Pred. No. 0.007; Matches 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NQSLEKVKAGQVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                          10 SLIIISVFLVGCAQN-----FSRQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%;
50.0%;
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Best Local Similarity 50.0°
Matches 20; Conservative
   A, Molecule type: DNA
A; Residues: 1-155 < BAE>
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hypothetical protein CC3073 [imported] - Caulobacter crescentus
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R;Micrman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J.; Ernolaeve, M.; Wilte, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Froc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.
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SLYB ECOLI
SLYB SALTY
PCP HAEIN
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HEM1 MYCLE
CANS RABIT
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Listing first 45 summaries
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BOVIN
BACSU
BACSU
SALTY
CAEEL
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Gapop 10.0 , Gapext 0.5
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OSMB
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Maximum DB seq length: 2000000000
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Match Length
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294.5
284.5
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113.5
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105.5
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                  P15999 rattus norv
P25705 homo sapien
P13445 homo sapien
P19483 bos taurus
003265 mus musculu
P18538 marek's dis
P37665 escherichia
088456 mus musculu
P14539 plasmodium
P13815 plasmodium
P12405 anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Madrid E;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of a genus-common rickettsial antigen
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Madrid E;
MEDLINE-290139499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Estksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M28482; AAA26378.1; ALT_SEQ.
EMBL; AJ235273; CAA15258.1; -
PRS; D33971; D33971.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia prowazekii.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=782,
  P19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.4%; Score 296; DB 1; Length 159; 38.1%; Pred. No. 1.5e-18; tive 30; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 19 17 kDa SURFACE ANTIGEN.
20 20 20 N-ACYL DIGLYCERIDE (PRODABLE)
159 AA; 16672 MW; A33D404B65EEB071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                      ATPA_RAT
ATPA_HUMAN
KICJ_HUMAN
ATPO_BOVIN
ATPA_MOUSE
VIB_HSWMD
YIAD_ECOLI
YIAD_ECOLI
CANS_MOUSE
CSP_FILMAN
ATPA_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 171:5199-5201(1989)
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Best Local Similarity 38.1
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-R.rickettsii;
MEDLINE-87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu z.Y., Bellini W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 170:4493-4500(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098 (2001).
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21R; A33971; A33971.
21R; A33971; B33971.
21R; A33971; B33971.
21R; G97860; G97860.
21R; PSO0113; PROKAR LIPOPROTEIN; 1.
21R; PSO0113; PROKAR LIPOPROTEIN; 1.
21R; PSO0113; PROKAR LIPOPROTEIN; 1.
21R; PSO0113; PROKAR LIPOPROTEIN; Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-30 FROM N.A.
SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=1139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii: transcription and posttranslational modification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                           Rickettsiaceae; Rickettsia; Alphaproteobacteria; Rickettsiales;
NCBL TaxID=781, 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
N -> D (IN REF. 3).
                    01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         SPECIES=R.conorii, and R.rickettsii;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES=R.conorii; STRAIN=Malish 7;
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EMBL; M26480; AAA26376.1; -.
EMBL; M26486; AAL03825.1; -.
EMBL; M16486; AAA26381.1; -.
EMBL; J03371; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rickettsii.";
J. Bacteriol. 169:2385-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 171:5199-5201(1989)
                                                                                                              17 kDa surface antigen precursor.
OMP OR RC1287.
                                                                                                                                                               Rickettsia conorii, and
Rickettsia rickettsii.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anchor (Probable).
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159
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PIR; A31836; A31836
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                              65 AVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY---- 119
                                                                                                                 64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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  63
                                                       64
                                  9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SKIMIJALATSMLOACNGPGGMNKOGTGTLLGGAGGALLGSOFGKGTGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
  SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Clin. Microbiol. 33:487-489(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=YH;

BULINRE-5229950; PubMed=7714214;

Furuya Y., Katayama T., Yoshida Y., Kaiho I.;

"Specific amplification of Rickettsia japonica DNA from clinical apecimens by PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Professateria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsiaae, Rickettsia.
NCBI TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 159;
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17 KDB SURRADE ANTIGEN.
ACYL DIGLYCERIDE (PROBABLE)
CDDCE7CEBDCD6B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Indels
                                                                                                                                                                                                                         120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS 159
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
17 kDa surface antigen precursor.
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Best Local Similarity
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Q52764;
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                                                                                                                                                                                                                                                       65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
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                                                                                                                                                9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-8935171; PubMed=2768201;
Anderson B.E., Talanabos T.;
"Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=785;
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    G -> E (IN REF. 3).
; 206A2BBF74FCE169 CRC64;
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20 20 N-ACYL DIGLYCERIDE (PROBAI
159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
                                                                                                                                                                                                                                                                                                                 120 QERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS 159
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                                                                                                       26;
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                                                              35.0%; Score 293; DB 1; 38.1%; Pred. No. 2.7e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) 17 kDa surface antigen precursor.
                                                                                                       29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
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                     16581 MW;
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                                                                                 Best_Local Similarity 38.19
Matches 61; Conservative
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nes 55; Conservative
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159
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                     159 AA;
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CONFLICT
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P22882;
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                                                                                                                                                                                                                                                                                                                                                   Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 15967 MW; B3AA833346FAC320 CRC64;
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Pred. No. 7.4e-17;
                                                (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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38.1%; Pred. No. /...
''ve 27; Mismatches
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01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
154 AA
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17 kDa surface antigen precursor (Fragment)
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(Rel. 34, Last seq
(Rel. 34, Last anno
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STANDARD;
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Best Local
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P50931;
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                      Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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Bacteria, Froteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsiae, Rickettsia.
NCBI_TaxID=35792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 263; DB 1; Length 154; 36.8%; Pred. No. 9.5e-16; Live 27; Mismatches 57; Indels 1
                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 1 19 PY SIMILARITY.

CHAIN 20 >154 IY ABA SURRACE ANTIGEN.

LIPID 20 10 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 154
154 AA; 15879 MW; E4FBE4C29D943581 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
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PROSTIE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
STGNAL.

1 19 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                  EMBL; U11013; AAB07704.1; -.
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STRAIN=MO 85-1084;
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                                                                                                                                                                                                                                                                                                                                                                                                64 GLIGSKIGOSMDQODK----IKUNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYORYNK 119
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                                                                                                                                                  , Score 261; DB 1; Length 154;
; Pred. No. 1.4e-15;
28; Mismatches 57; Indels 14;
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Rickettsiaceae, Rickettsieae, Rickettsia.
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SIGNAL.
1 19 BY SIMILARITY.
20 >154 17 kDa SURFACE ANTIGEN.
LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
   17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
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20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 NW, OCF85AD5D96DFEFB CRC64;
20 >154 17 KDa SUKFACE ANTICUL.
20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 SD06F45F9DBD5EEC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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                                                                                                                                                     31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 GQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azad A.F., Sacci J.B. Jr., Nelson W.M., Dasch G.A.,
Schmidtmann B.T., Carl M.;
"Genetic characterization and transovarial transmission of a
typhus-like rickettraia found in cat fleas.";
Proc. Natl. Acad. Sci. U.S.A. 89-43-46(1992).
--- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 51872 / WA-C / Serotype 0:8;
STRAIN=ATCC 51872 / WA-C / Serotype 0:8;
STRAIN=ATCC 51872 / WA-C / Serotype 0:8;
Bachiner A.J., Hancke W.G.;
"A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli.";
"Bacteriol. 174-11029-1035 (1922).
-1- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.
-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.8%; Score 157; DB 1; Length 80; 40.3%; Pred. No. 5.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA; 8372 MW; AD289A48EAB19E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M82879; -; NOT ANNOTATED CDS.
InterPro; IPR000437; Prok lipoprot.
PROSITE; PS00013; PROKAR LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation update)
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MEDLINE=92108069; PubMed=1729713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 NPDTGNSYSVEPVRTYQ 115
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(Rel. 26, Last seq
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Enterobacteriaceae, Yersinia.
NCBI_TaxID=630;
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                                                                                                                                                            anchor (Probable)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Or Send...

EMBL; U1017; AAB07705.1; -.

EMBL; U1017; AAB07705.1; -.

PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antignal.

SIGNAL 1 19 BY SIMILARITY.

20 >154 17 kDa SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 30.9%; Score 258; DB 1; Length 15
1 Similarity 36.1%; Pred. No. 2.5e-15;
56; Conservative 28; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
120 RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR 154
                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kba surface antigen precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ohio 83-441;
                                                                                                                                                                                                                                                                                    Rickettsia montana.
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Best Local Similarity
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                                                                                                              17KD RICMO
P50929;
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17KD_RICCA
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                                                                                                                                                           10 SLIIISVFLVGCAQN-----PSRQE------VGAAT 34
                                                                                                                                                                                  7 AVAİAAVTLIGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=E.coli;
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-E.coli; STRAIN-K12 / MG1655; MBDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Maceror J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97251357; Pubbled=907039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Kotomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horluchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome
a 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                    51;
                                                                                                            DB 1; Length 155;
                                                          OUTER MEMBRANE LIPOPROTEIN PCP. N-ACYL DIGLYCERIDE (POTENTIAL).
                                                                                                                                                                                                           35 GAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                    Indels
                                                                                    155 AA; 15362 MW; 8AD6BE2132E849FA CRC64;
                                                                                                 13.6%; Score 113.5; DB 1;
24.7%; Pred. No. 0.0053;
Micmatches 43;
                                                                                                                                                                                                                                                                                                                                                       P55741; P76183;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
older membrane lipoprotein slyB precursor.
SLYB OR B1641 OR Z2655 OR ECS2350 OR SF1668.
                                                                                                                                                                                                                                                          --NOSLEKVKAGQVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                                                                                              155 AA
                                                                                                                                                                                                                                                                         127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
     EMBL; ANDTE, 23787.
PIR; S23787, S23787.
PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal.
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli,
Escherichia coli 0157:H7, and
EMBL; X60448; CAA42977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12;
                                                                                                          Query Match
Best Local Similarity 24.7'
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                             155
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               SLYB ECOLI
                                                                          LIPID
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-E.coli; STRAIN=0157.H7 / RIMD 0509952;
MEDLINE=21156211; PubMed=11258706;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hatcori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 MYGLSLVĞCVNNDTLSGDVYTASEAKQVQNVSYGTIVNVRPVQIQGGDDSNVIGAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-S flexner; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin M., Wang Y., Shen Y., Lu W., Wang J., Liu H., Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang J., Yang G., Wu H., Qu D., Dong J., Yang J., Xue Y., Zhang X., Zhang Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                              Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; P90922; FULLED PROTEIN; 1.

ECGENE; EG1409; S1yB.

ECGENE; EG1409; S1yB.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

OUTER MEMBRANE LIPOPROTEIN SLYB.

SIGNAL 1 17 OUTER MEMBRANE LIPOPROTEIN SLYB.

CHAIN 18 18 N-ACYL DIGLYCERIDE.

TT IN REF. 2).

TT TOTD 2 98 A -> T (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anchor (Potential).
-!- SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE PCP AND
Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                     SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.025;
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EMBL; AP002558; BAB35773.1; --
EMBL; AE015187; AAN43250.1; --
PIR; B85771; B85771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:529-533(2001).
Res. 3:363-377(1996)
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Best Local Similarity
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34; Conservative
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P10325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                      VGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRW 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES S. (Yphimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINB=21534948; PubMed=11677609;
MCCIelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Potential).
-!- SIMILARITY: TO E.COLI SLYB, H.INFLUENZAE PCP AND Y.ENTEROCOLITICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhimurium;
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain C. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-cr membrane lipoprotein slyB precursor.
SLYB OR STM1445 OR STY1677 OR T1313.
                                                                                                                    RNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                  --- DDGNTIMVVQKQGNTRFSPGQR 140
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MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                          STANDARD;
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Socott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane; Lipoprotéin; Signal; Complete proteome.
SIGNAL 1 17 POTENTIAL.
CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN SLYB.
LIPID 18 18 N-ACYL DIGLYCERIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 105.5; DB 1; Length 155;
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EMBL, AL627271; CAD01922.1; --
EMBL, AE016838; AA068963.1; --
Stydens; SGL0573; B1yB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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and assembly of Haemophilus influenzae
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SPECIES=E.coli; STRAIN=K12;
MEDLINE=97061202; PubMed=8905122;
MEDLINE=97061202; PubMed=8905122;
MEDLINE=97061202; PubMed=8905122;
Oshima T., Aiba H., Baha T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inda T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SPECIES=E.CO11; STRAIN=K12 / MG1655;
BHEDLINE=97426617; PubMed=9279503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Greegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                    -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 VGAATGAVVGGVAGOLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL 82
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CSLVAEFVF -> VAGRRVRI (IN REF. 1).
D7880327FCF0C985 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 12.2%; Score 102; DB 1; Length 155; 1 Similarity 39.6%; Pred. No. 0.051; 21; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                               -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; H11579; -.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
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NCBI_TaxID=562, 217992, 623;
    "Whole-genome random sequencing
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EMBL; U32832; AAC23228.1; -.
PIR; I64130; I64130.
                                                                                                                                         Y.ENTEROCOLITICA PCP.
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Escherichia coli 06, and
                                               Science 269:496-512(1995)
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SPECUESE. Coll; STRAIN=K12;
SPECUESE. Coll; STRAIN=K12;
WEDLINE=81236546; PubMed=6565208;
Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.;
Young J.G., Rogers B.L., the respiratory NADH dehydrogenase of Escherichia coll: UNG initiation codon.";
Escherichia coll: 116:165-170(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res, 30:4432-4441(2002).
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SPECIES=E.coli; STRIN-06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
MayNew G.F., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
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Nucleic Acids Res. 22:4756-4767(1994).
-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                            of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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EMBL; V00306; -; NOT_ANNOTATED_CDS.
EMBL, AE015138; AAN42732.1; ALT_INIT.
PIR; C64855; C64855.
EcoGene; EG12444; ycfJ.
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MEDLINE=95075659; PubMed=7984428;
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"Identification of a genus-common Rickettsial surface antigen in the salmonid pathogen Placitickettsia salmonis.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

SEMBL, AF184152; AAG17000.1; -.
SEQUENCE 162 AA; 17661 MW; DDB9986FD94A527B CRC64;
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Piscirickettsiaceae, Piscirickettsia.
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                            NCBI_TaxID=1238;
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG20452.1; -.
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;
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MEDLINE=21217364; PubMed=11321078;
Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98087556; PubMed=9425244;
MEDLINE=98087556; PubMed=9425244;
Bavis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
Curr. Microbiol. 36:80-84(1998).
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                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=789;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                            148 AA; 15050 MW; A7AFEEFDE0AEEE4C CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                     Query Match 37.5%; Score 313.5; DB 2; Best Local Similarity 41.6%; Pred. No. 1.8e-20; Matches 57; Conservative 29; Mismatches 42;
                           148 AA.
                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 kDa genus-common antigen.
Rickettsia felis (Rickettsia azadi).
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                                                                                          17 kDa common-antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 EIYGTACROPDGRWQVI 158
                                                 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                   U76907; AAC02809.1; -.
                        PRELIMINARY;
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                                                                                                         Rickettsia sp.
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64 GLIGSKIGQSMDQQDK---IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                       65 AVLGGQIGAGMDEQDRRLAELTSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY---- 119
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"Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1; -.
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Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Schulenburg H.J.G.V.D., Majerus M.E.N.;
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"On the evolution of male-killing: Monophyletic origin and horizontal
transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
(Coleoptera: Coccinellidae) ";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269518; CAB96383.1; -.
EMBL; AJ269517; CAB96382.1; -.
NON TER 144 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 kba antigen (Fragment).
Rickettsia cooleyi.
Bacterrai, Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsiaceae; Rickettsiaceae; Rickettsiaceae; NCBI_TaxID=69410;
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male-killing Rickettsia from Adalia bipunctata.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=38028;
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                                                                                                                                                                                          120 QERRQQYCREFQQXAMIAGQXQEIYGTACRQPDGRWQVIS 159
                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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39.6%; Pred. No. 2.6e-16;
tive 23; Mismatches 49
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nes 53; Conservative
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64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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MEDLINE=93084757; PubMed=1452660;

Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyer B.;

Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyer B.;

Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyer B.;

Britan and Comparison of Australian human spotted fever group rickettsiae.";

J. Clin. Microbiol. 30:2896-2902(1992).

EMBL: M99391; AAA73386.1;
                                                                                                                                  WEDLINE=20575219; PubMed=11133455; Sloggett J.J., Webberley M.K., Schlienburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Bertrand D., Hurst G.D.D., Majerus M.E.N.; Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera: Appl. Environ. Microbiol. 67:270-277(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                 9
                male-killing Ricketűsia from Adalia decempunctata.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 259.5; DB 2; Length 144; 39.7%; Pred. No. 1.2e-15; ive 22; Mismatches 48; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
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                                                                                                                                                                                                                                                                                                                   144 144
144 AA; 14801 MW; C825472F16A56AE7 CRC64;
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01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-NOV-1902 (TrEMBLrel. 22, Last annotation update)
(Clone PRB FISF 1), 5' end CDS (Fragment).
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Beet Local Similarity 39.7%,
Trines 52; Conservative 2
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    kDa antigen (Fragment)
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132 KSYGNACRQPD 142
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                                                                             NCBI_TaxID=120393;
                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                          10 NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 69
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                                                                                                                  26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
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MEDLINE 99045882; PubMed-9828442;
Stenos J., Raoult D.;
Stenos J., Rouv V., Walker D., Raoult D.;
Ricketteia hone; pp. nov., the aetiological agent of Flinders Island spotted fever in Australia.";
Int. J. Syet. Bacteriol. 48:1399-1404(1998).
EMBL; AF0677124; AAB1846.1; -.
EMBL; AF060706; AAD20231.1; -.
EMBL; AF060704; AAD20230.1; -.
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                                                                               Gaps
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                                        Length 144;
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Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
14785 MW; C8254739CCA56AE7 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (17 kDa protein) (Fragment).
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Last sequence update)
Last annotation update)
                                    31.2%; Score 260.5; DB 2;
39.7%; Pred. No. 9.5e-16;
tive 22; Mismatches 48;
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Q9K4W8;
01-OCT-2000 (TEMBLE1 15,
01-OCT-2000 (TEMBLE1 15,
01-OCT-2002 (TEMBLE1 22,
                                                                           52; Conservative
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132 KAYGNACRQPD 142
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125 KAYGNACROPD 135
  144 AA;
                                    Query Match
Best Local Similarity
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SEQUENCE
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26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK---IK 81
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Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427882; CAD20878.1; -.
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                                                                                                                                                                                                                                  142 EIYGTAC 148
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125 KAYGNAC 131
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STRAIN=California 2;
Raoult D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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"First detection of spotted fever group rickettsiae in Ixodes ricinus
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MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.5%; Score 247; DB 2; Length 151; Best Local Similarity 36.2%; Pred. No. 1.6e-14; Matches 55; Conservative 26; Mismatches 57; Indels 14;
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                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=35789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia sp. IrITA3.
Bacteria, Foteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=184232;
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Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
rickettsiosis...;
submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFISIO35; AAG09427.1; -..
NON_TER 151 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AA; 15621 MW; B77407B9C71E4B39 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
125 QD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154
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                                                                                                                                               151 AA
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01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Outer membrane protein (Fragment).
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Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427883; CAD20879.1;
                                                                                                                                            PRT;
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                                                                                                                                         PRELIMINARY;
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82 INQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
                                                                                                                                      10 SQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ 124
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10 NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genchi C.; "First detection of spotted fever group rickettsiae in Ixodes ricinus
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184231;
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Rickettsia sp. California 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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131 AA

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PRELIMINARY;
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Q9L522;
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EMBL; U04162; AAA19235.1; -.
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Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Stouthamer R.,
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 131;
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Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.4%; Score 237.5; DB 2; Length Best Local Similarity 37.8%; Pred. No. 9.8e-14; Matches 48; Conservative 22; Mismatches 48; Indels
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                                                                                 SEQUENCE FROM N.A.
STRAIN=California 2;
Roux V., Raoult D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
"A new SFG rickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                       131 AA; 13374 MW; 23C8819B29FFF860 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (Fragment).
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125 KAYGNAC 131
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82 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
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Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
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BMBL; AF266571; AAF69012.1; -. NON_TER
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01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 Aba surface antigen (Fragment).
Rickettsia peacockii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsiaees; Rickettsiaees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 28.3%; Score 236.5; DB 2; Length 131; Local Similarity 37.8%; Pred. No. 1.2e-13; ne 48; Conservative 22; Mismatches 48; Indels 9.
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                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
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...vi-zuuz (TrEMBLrel. 22, Created)
1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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EMBL; AJ427881; CAD20877.1; -.
NON TER 1
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                                                                                                                                                                                 Rickettsia helvetica
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125 KAYGNAC 131
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¹⁴² EIYGTAC 148 : || || 125 KAYGNAC 131

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